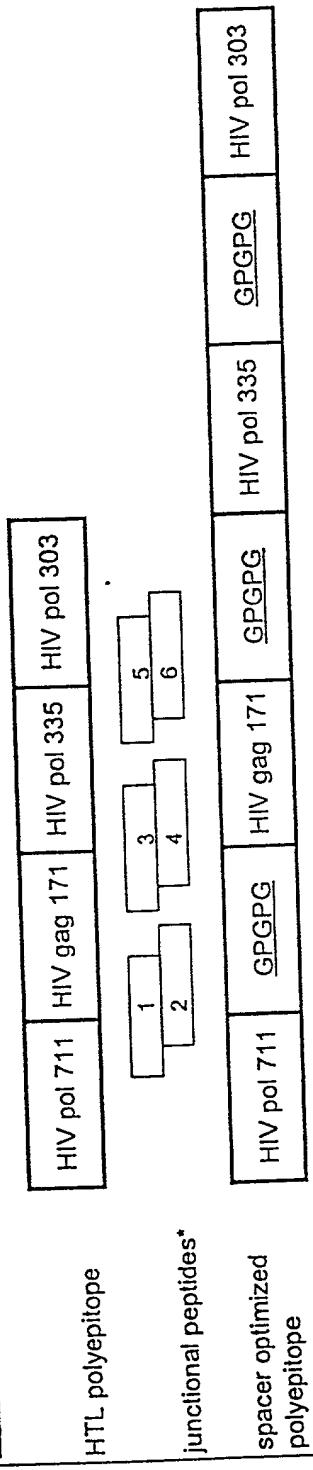


Figure 1. Immunogenicity of HIV- and HCV-derived minigenes in HLA transgenic animals.

Magnitude of CTL responses are stored as follows + up to 2 LU (lytic units) or 10 SU (cytotoxic units); ++ up to 20 LU or 100 SU; + + + up to more than 200 LU or 1000 SU. Magnitude + represents number of independent cultures yielding positive responses.

FIGURE 1

Figure 2a. Synthetic polypeptides encoding HIV-derived HTL epitopes



* junctional peptides comprise either 10 amino acids from the N-terminal epitope and 5 amino acids from the C-terminal epitope or 5 amino acids from the N-terminal epitope and 10 amino acids from the C-terminal epitope.

Figure 2b. Proliferative responses to synthetic polypeptides encoding HIV-derived HTL

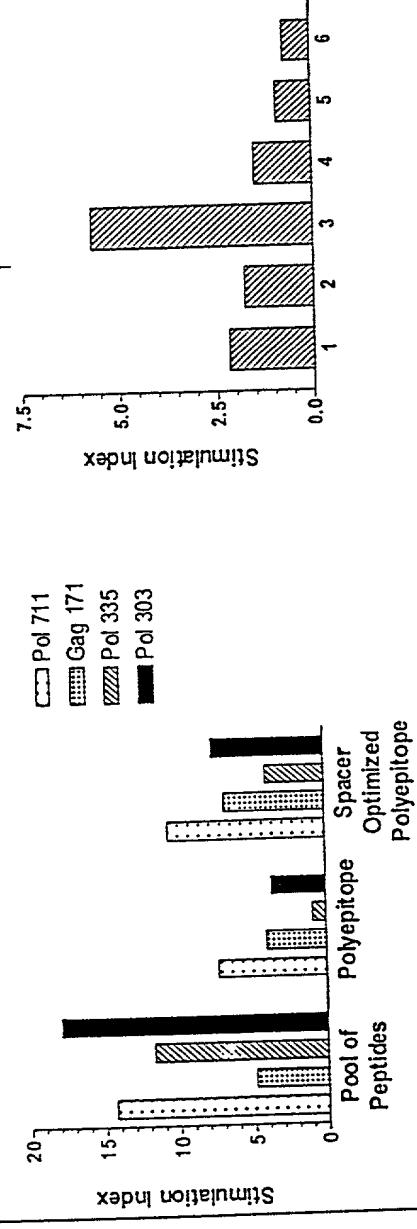
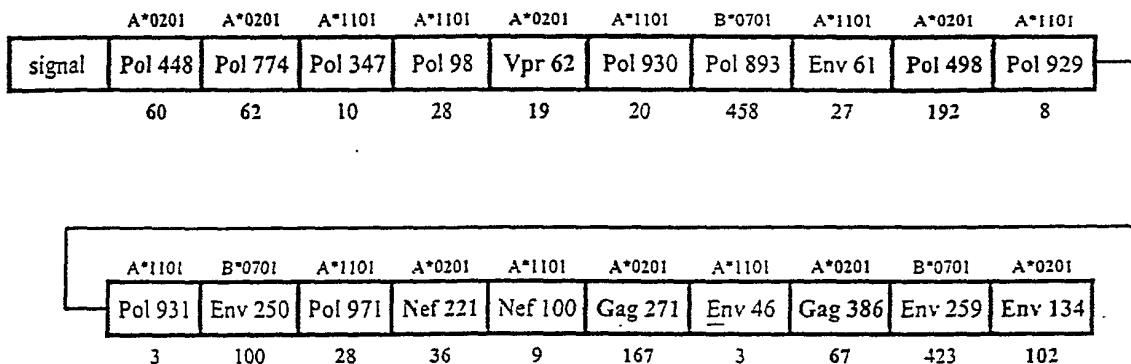


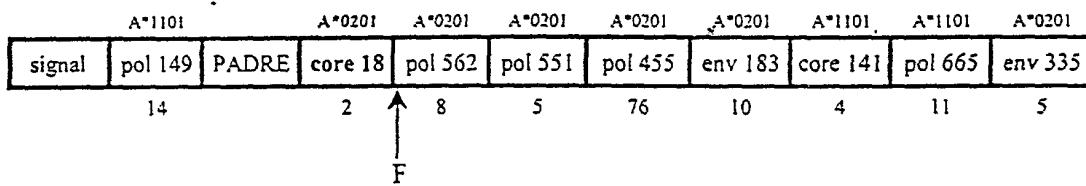
FIGURE 2

a : HIV-FT

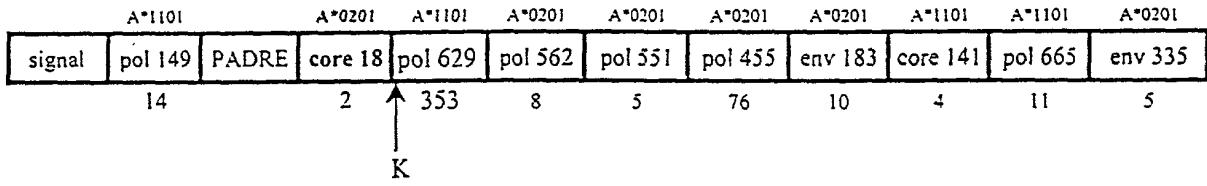


b : HBV-specific multiepitope constructs

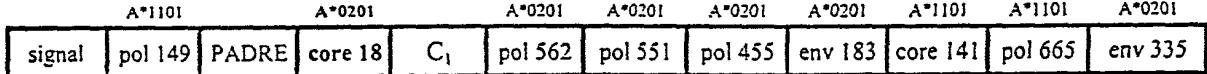
HBV.1



HBV.2



HBV.1X



C₁= either W, Y, L, K, R, C, N or G

FIGURE 3

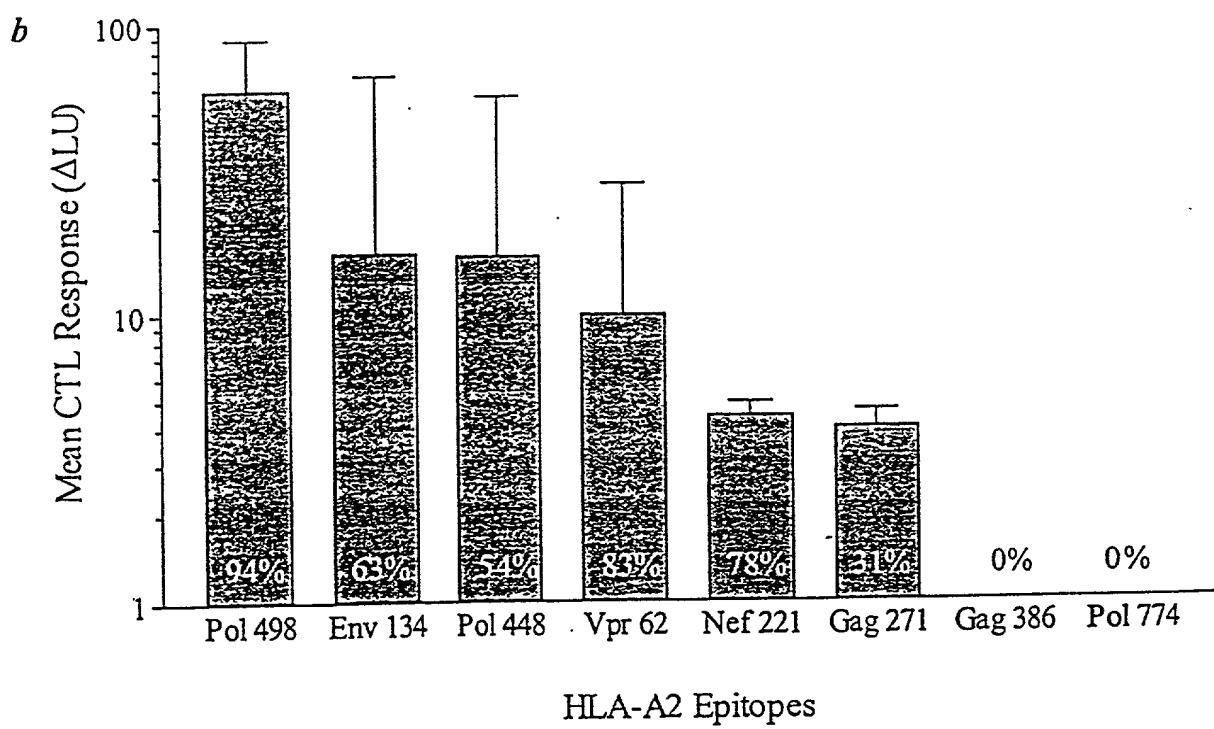
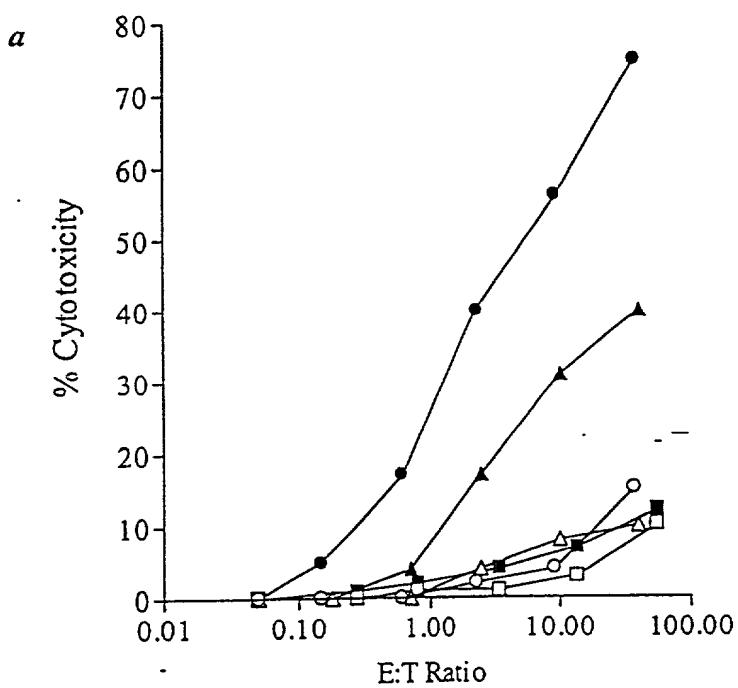


FIGURE 4

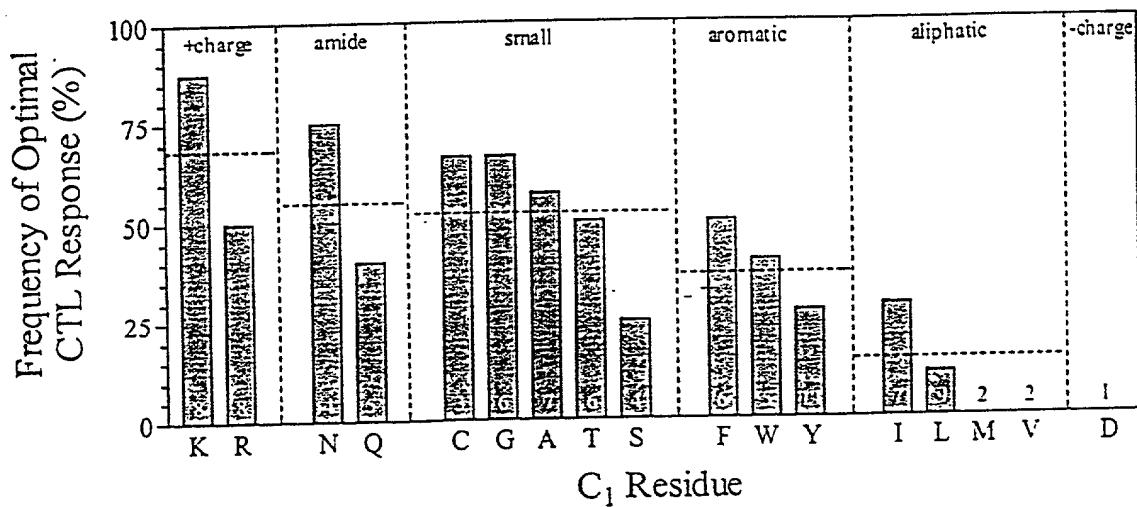
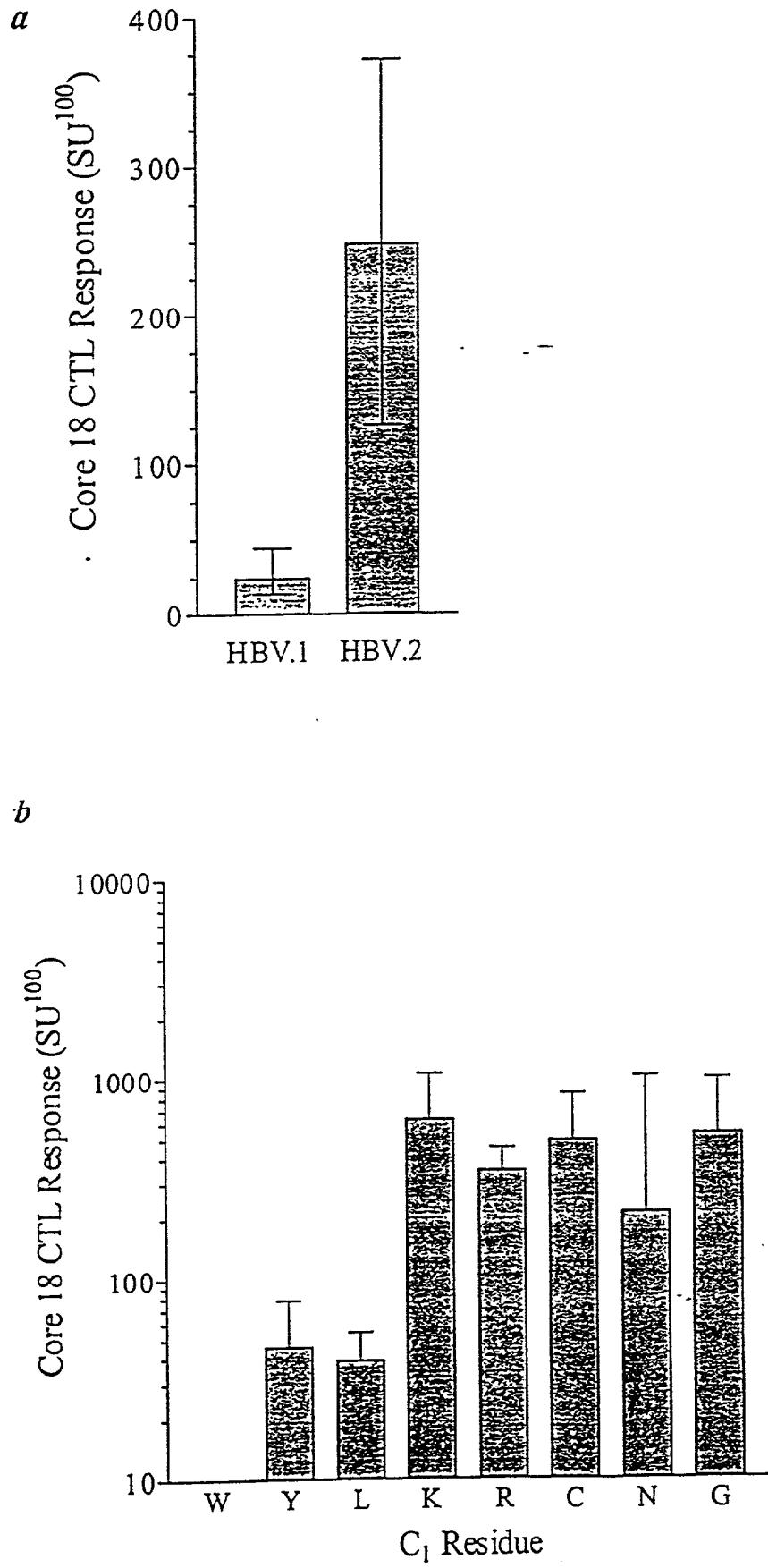


FIGURE 5

FIGURE 6



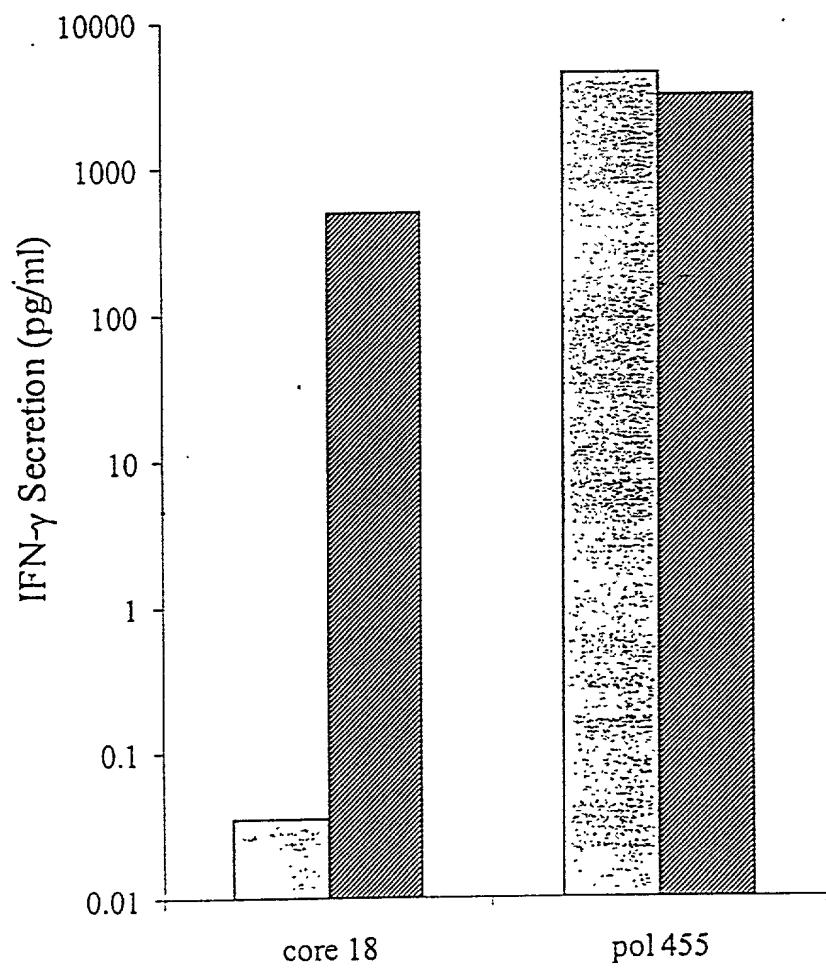


FIGURE 7

File X2000 in Z:\Dokumente\G

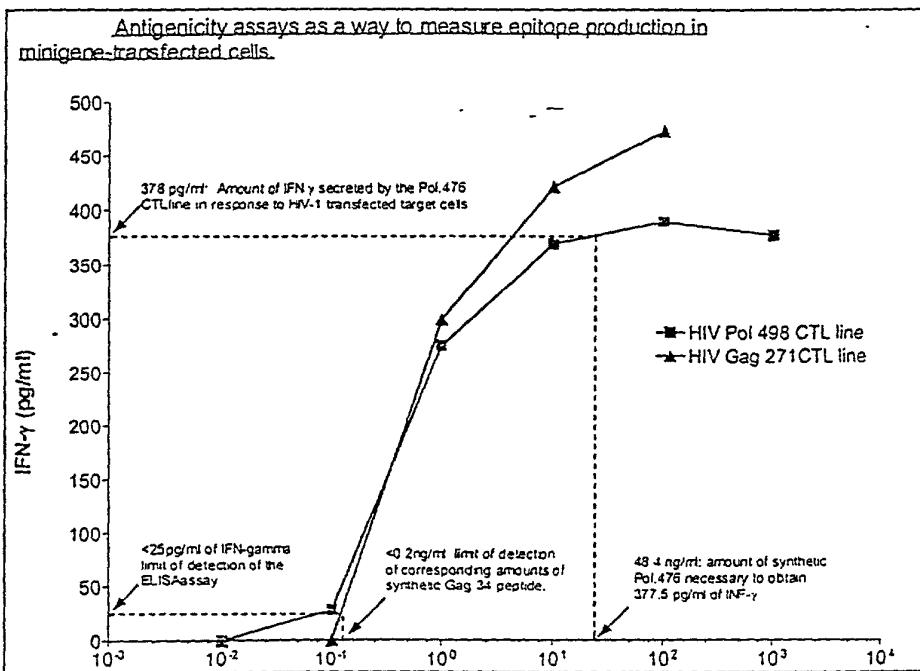


FIGURE 8

EP-HIV-1090

	Δ^{*101}	Δ^{*201}	Δ^{*301}	Δ^{*401}	Δ^{*501}	Δ^{*601}	Δ^{*701}	Δ^{*801}	Δ^{*901}	Δ^{*1001}
signal	pol 448 x	pol 498 x	env 250 x	env 259 x	PADRE x	ref 94 x	env 134 x	GAA	pol 306 x	pol 347 x
									env 61 x	

HIV-CPT

	Δ^{*101}	Δ^{*1101}	Δ^{*201}	Δ^{*301}	Δ^{*401}	Δ^{*501}	Δ^{*601}	Δ^{*701}	Δ^{*801}	Δ^{*901}	Δ^{*1001}
signal	env 250 x	pol 971 x	pol 98 x	PADRE x	ref 221 x	env 545 x	ref 547 x	env 62 x	pol 971 x	pol 98 x	env 75 x
											gap 271 x

HIV-TC

	Δ^{*102}	Δ^{*101}	Δ^{*201}	Δ^{*301}	Δ^{*401}	Δ^{*501}	Δ^{*601}	Δ^{*701}	Δ^{*801}	Δ^{*901}	Δ^{*1001}
signal	pol 597 x	pol 347 x	Env 722 x	Env 250 x	Env 250 x	Env 237 x	Env 237 x	Env 62 x	Env 62 x	Env 62 x	Env 62 x

	Δ^{*202}	Δ^{*101}	Δ^{*201}	Δ^{*301}	Δ^{*401}	Δ^{*501}	Δ^{*601}	Δ^{*701}	Δ^{*801}	Δ^{*901}	Δ^{*1001}
signal	Env 221 x	gap 366 x	vpr 62 x	AAA	env 47 x	env 47 x	env 545 x	env 61 x	pol 448 x	ref 94 x	gap 271 x

	Δ^{*203}	Δ^{*101}	Δ^{*201}	Δ^{*301}	Δ^{*401}	Δ^{*501}	Δ^{*601}	Δ^{*701}	Δ^{*801}	Δ^{*901}	Δ^{*1001}
signal	pol 597 x	Env 466 x	Env 100 x	Env 295 x	Env 61 x	Env 61 x	Env 237 x	Env 244 x	Env 75 x	Env 893 x	Env 651 x

	Δ^{*204}	Δ^{*101}	Δ^{*201}	Δ^{*301}	Δ^{*401}	Δ^{*501}	Δ^{*601}	Δ^{*701}	Δ^{*801}	Δ^{*901}	Δ^{*1001}
signal	Env 498 x	Env 186 x	Env 55 x	Env 55 x	Env 55 x	Env 55 x	Env 83 x	Env 84 x	Env 259 x	Env 658 x	Env 929 x

	Δ^{*205}	Δ^{*101}	Δ^{*201}	Δ^{*301}	Δ^{*401}	Δ^{*501}	Δ^{*601}	Δ^{*701}	Δ^{*801}	Δ^{*901}	Δ^{*1001}
signal	Env 47 x	Vpr 14 x	Env 921 x	Env 921 x	Env 921 x	Env 921 x	VII7 x	Env 134 x	Env 134 x	Env 163 x	

FIGURE 9

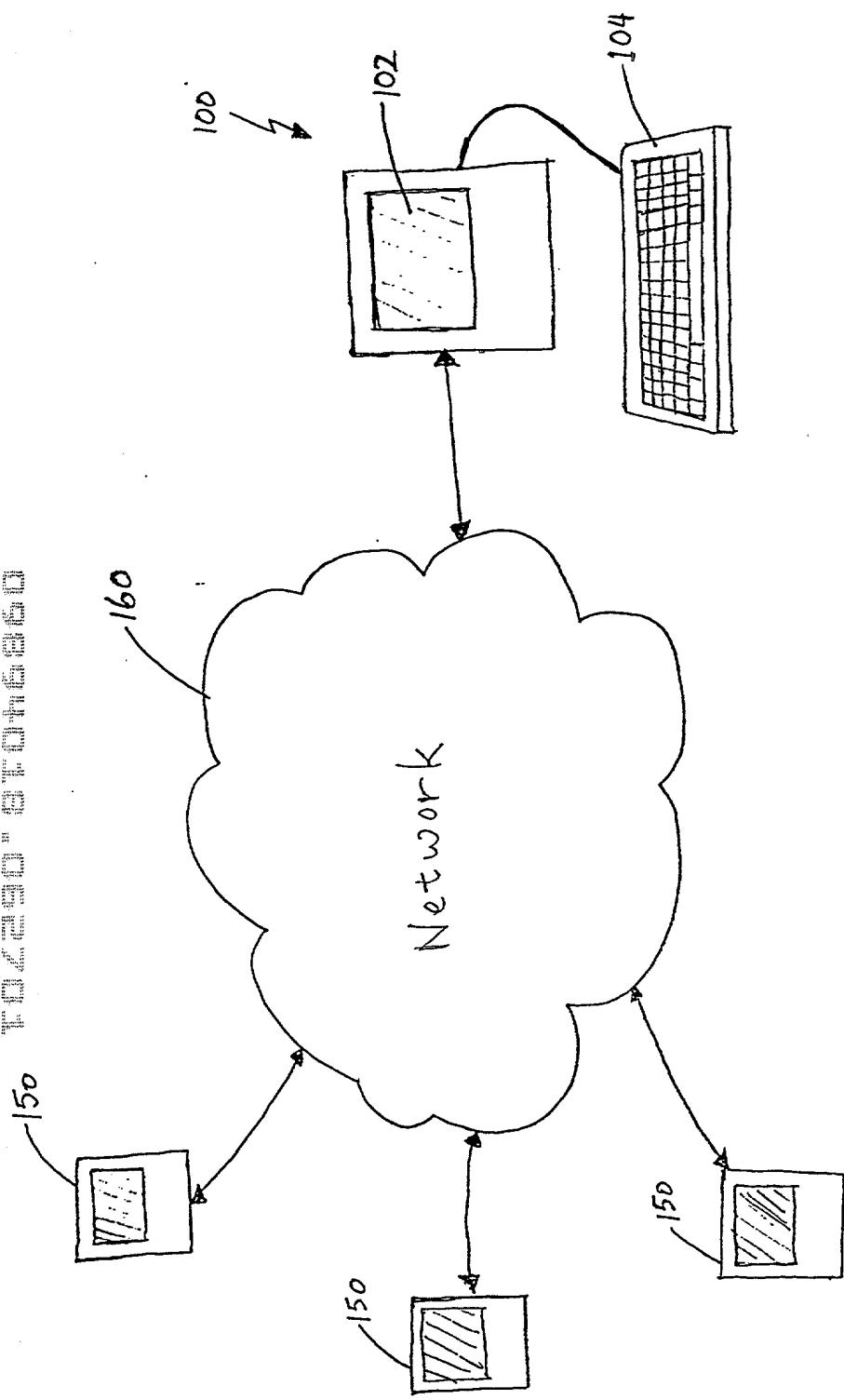


FIGURE 10

<u>Sequence</u>	<u>Length</u>	<u>Code</u>
VLAEAMSQV	9	A
ILKEPVHGV	9	B
TLNFPISPI	9	C
SLLNATDIAV	10	D
QMAVFIHNFK	10	E
VTVYYGVPVWK	11	F
FPVRPQVPL	9	G
YPLASLRSLF	10	H
VIYQYMDDLY	10	I
IYQEPMKNL	9	J
IWGCSGKLI	9	K

200

<u>AA</u>	<u>C+1 ranking</u>	<u>N-1 ranking</u>
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

202

Motif Specification

XXXX(FY)XX(LIMV)
 XXXX(FY)XXX(LIMV)
 XXXXXNXXXX(LIMV)
 XXXXXNXXXX(LIMV)
 X(LM)XXXXXXV
 X(LM)XXXXXXXV
 X(LMVT)XXXXXXX(KRY)
 X(LMVT)XXXXXXX(KRY)
 XPXXXXXX(LIMVF)
 XPXXXXXXX(LIMVF)

206

FIGURE 11A

MaxInsertions={enter value here} 208
OutputToScreen=yes/no 210
OutputToFile=yes/no 212
MinimumAccepted={enter value here} 214
MaxDuplicateFunctionValues={enter value here} 216
MaxSearchTime (min.)={enter value here} 218
Exhaustive=yes/no 220
NumStochasticProbes={enter value here} 222
MaxHitsPerProbe={enter value here} 224
RandomProbeStart=yes/no 226

FIGURE 11B

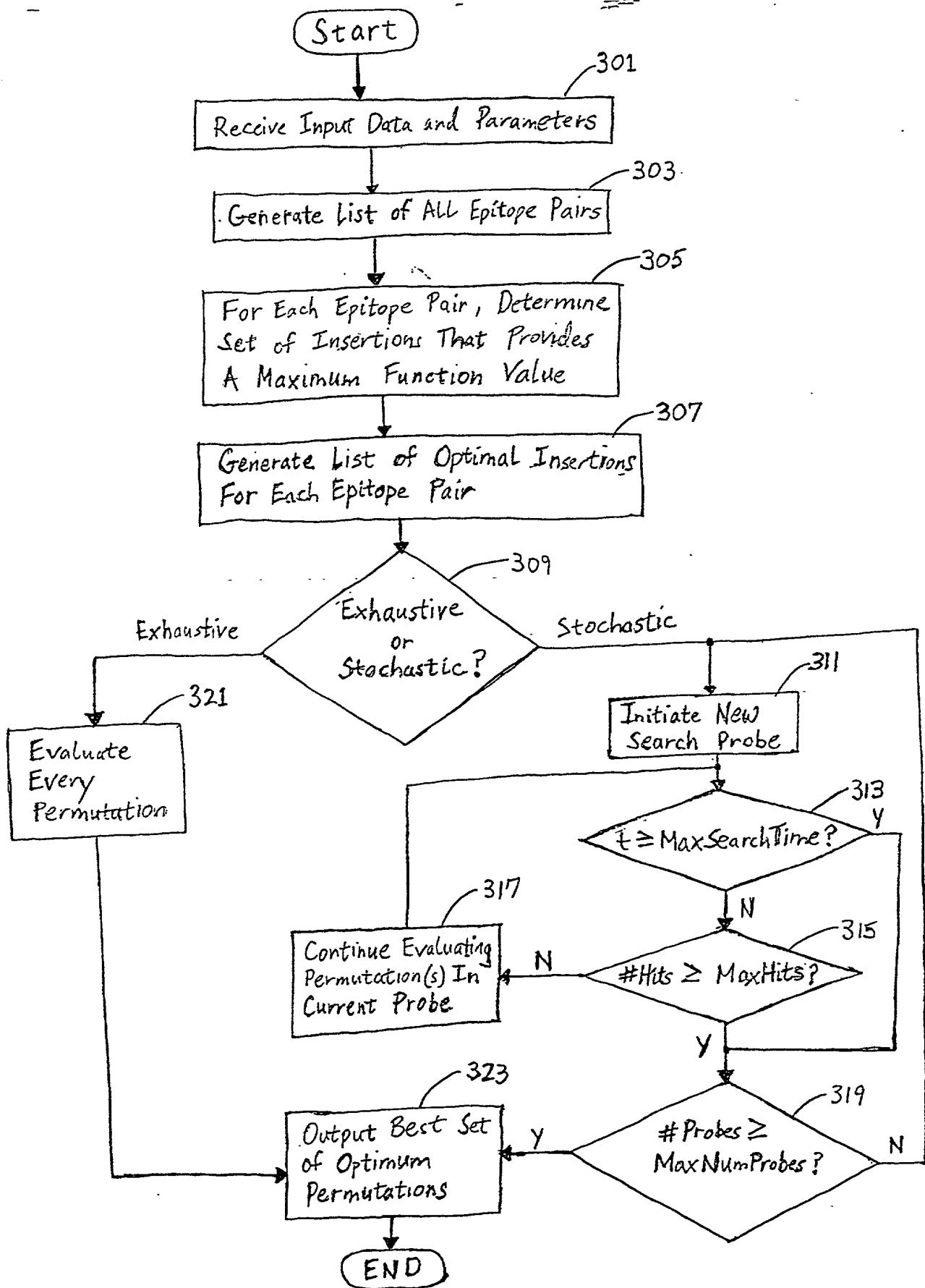


FIGURE 12

Junctional Analyzer run on Saturday, February 26, 2000 09:06:23 pm.

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.33
G	1.33	1.80
I	0.50	0.86
K	0.64	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

204

The following 10 motif specifications will be used to search for junctionals.

Count	Motif Specification
1	XXXX(FY)XX(LIMV)
2	XXXX(FY)XXX(LIMV)
3	XXXXNXXXX(LIMV)
4	XXXXNXXXX(LIMV)
5	X(LM)XXXXXXV
6	X(LM)XXXXXXXXV
7	X(LMVT)XXXXXX(KRY)
8	X(LMVT)XXXXXXX(KRY)
9	XPXXXXXX(LIMVF)
10	XPXXXXXX(LIMVF)

206

Code	Peptide	Length
A	VLAEAMSQV	9
B	ILKEPVHGV	9
C	TLNFPISPI	9
D	SLLNATDIAV	10
E	QMAVFIHNFK	10
F	VTVYYGVPWK	11
G	FPVRPQVPL	9
H	YPLASLRSLF	10
I	VIYQYMDDLY	10
J	IYQEPFKNL	9
K	IWGCSGKLI	9

202

MaxInsertions = 4 (208)

FIGURE 13A

OutputToScreen = No

OutputToFile = Yes

MinimumValueAccepted = 0

MaxDuplicateFunctionValues = 50

SearchTime = 5

NumStochasticProbes = 10

MaxHitsPerProbe = 25

RandomProbeStart = Yes

Col. 1 Code 1	Col. 2 I1	Col. 3 I2	Col. 4 I3	Col. 5 I4	Col. 6 Code 2	Col. 7 C	Col. 8 N	Col. 9 C+N	Col. 10 J	Col. 11 MaxFunc.
A	C	A		L	B	2.00	2.20	4.40	0	8.80
A	C			L	C	2.00	2.20	4.40	0	8.80
A	C			L	D	2.00	2.20	4.40	0	8.80
A	C			L	E	2.00	2.20	4.40	0	8.80
A	C			R	F	2.00	1.57	3.14	2	1.57
A	C			R	G	2.00	1.57	3.14	1	3.14
A	C			R	H	2.00	1.57	3.14	0	6.28
A	G				I	1.80	1.33	2.39	1	2.39
A	C	A	A	G	J	2.00	1.33	2.66	0	5.32
A	C			R	K	2.00	1.57	3.14	0	6.28
B	C	A	A	G	A	2.00	1.33	2.66	0	5.32
B	C	A		R	C	2.00	1.57	3.14	0	6.28
B	C	A		R	D	2.00	1.57	3.14	0	6.28
B	C	A	A	R	E	2.00	1.57	3.14	0	6.28
B	C	A	A	G	F	2.00	1.33	2.66	1	2.66
B	C			R	G	2.00	1.57	3.14	1	3.14
B	C			R	H	2.00	1.57	3.14	0	6.28
B	C	A	A	G	I	2.00	1.33	2.66	1	2.66
B	C	A	A	G	J	2.00	1.33	2.66	0	5.32
B	C	A	A	G	K	2.00	1.33	2.66	0	5.32
C	C	A		R	A	2.00	1.57	3.14	1	3.14
C	C	A		R	B	2.00	1.57	3.14	1	3.14
C	C	A		L	D	2.00	2.20	4.40	1	4.40
C	C	A		R	E	2.00	1.57	3.14	1	3.14
C	C			R	F	2.00	1.57	3.14	1	3.14
C	C			R	G	2.00	1.57	3.14	1	3.14
C	C			R	H	2.00	1.57	3.14	0	6.28
C	C	A		R	I	2.00	1.57	3.14	1	3.14
C	C	A	A	R	J	2.00	1.57	3.14	0	6.28
C	C	A	A	R	K	2.00	1.57	3.14	0	6.28

FIGURE 13B

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
D	C			L	A	2.00	2.20	4.40	0	8.80
D	C			LL	B	2.00	2.20	4.40	0	8.80
D	C			LL	C	2.00	2.20	4.40	0	8.80
D	C			L	E	2.00	2.20	4.40	0	8.80
D	G			F	1.80	1.33	2.39	0	4.79	
D	G			G	2.00	1.57	3.14	0	6.28	
D	C	A	A	H	2.00	1.33	2.66	0	5.32	
D	C	A	A	I	2.00	2.20	4.40	1	4.40	
D	C	A	A	J	2.00	1.33	2.66	0	5.32	
D	C	A	A	K	2.00	1.57	3.14	0	6.28	
D	C	A	A	A	2.00	2.20	4.40	0	8.80	
D	C	A	A	B	2.00	2.20	4.40	0	8.80	
D	C	A	A	C	2.00	2.20	4.40	0	8.80	
D	C	A	A	D	2.00	2.20	4.40	0	8.80	
D	C	A	A	F	2.00	1.57	3.14	0	6.28	
D	C	A	A	G	2.00	1.57	3.14	0	6.28	
D	C	A	A	H	2.00	1.57	3.14	0	6.28	
D	C	A	A	I	2.00	1.57	3.14	0	6.28	
D	C	A	A	J	2.00	1.57	3.14	0	6.28	
D	C	A	A	K	2.00	2.20	4.40	0	8.80	
D	C	A	A	A	2.00	1.57	3.14	0	6.28	
D	C	A	A	B	2.00	1.57	3.14	0	6.28	
D	C	A	A	C	2.00	1.57	3.14	0	6.28	
D	C	A	A	D	2.00	2.20	4.40	1	4.84	
D	C	A	A	F	2.00	1.33	2.93	1	2.93	
D	C	A	A	G	2.00	1.33	2.93	0	5.85	
D	C	A	A	H	2.00	1.33	2.93	0	5.85	
D	C	A	A	I	2.00	1.33	2.93	0	5.85	
D	C	A	A	J	2.00	1.33	2.93	1	2.93	
D	C	A	A	K	2.00	1.57	3.45	1	3.45	
D	C	A	A	A	2.00	1.57	3.45	0	6.91	
D	C	A	A	B	2.00	1.57	3.14	1	3.14	
D	C	A	A	C	2.00	1.57	3.14	2	1.57	
D	C	A	A	D	2.00	1.57	3.14	1	3.14	
D	C	A	A	E	2.00	2.20	4.40	1	4.40	
D	C	A	A	F	2.00	1.57	3.14	2	1.57	
D	C	A	A	G	2.00	2.20	4.40	4	1.10	
D	C	A	A	H	2.00	1.33	2.66	0	5.32	
D	C	A	A	I	2.00	1.57	3.14	2	1.57	
D	C	A	A	J	2.00	1.57	3.14	1	3.14	
D	C	A	A	K	2.00	1.33	2.66	0	6.28	
D	C	A	A	A	2.00	1.57	3.14	0	6.28	
D	C	A	A	B	2.00	1.57	3.14	0	5.32	
D	C	A	A	C	2.00	1.57	3.14	0	5.32	
D	C	A	A	D	2.00	1.57	3.14	0	5.32	
D	C	A	A	E	2.00	1.33	2.66	1	2.66	
D	C	A	A	F	2.00	1.33	2.66	0	5.32	
D	C	A	A	G	2.00	1.57	3.14	1	3.14	
D	C	A	A	H	2.00	1.33	2.66	1	2.66	
D	C	A	A	I	2.00	1.33	2.66	1	2.66	
D	C	A	A	J	2.00	1.33	2.66	1	2.66	
D	C	A	A	K	2.00	1.33	2.66	0	5.32	

FIGURE 13C

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
I	K	A	A	G	A	2.20	1.33	2.93	0	5.85
I	K	A	A	G	B	2.20	1.33	2.93	1	2.93
I	K	A	A	G	C	2.20	1.33	2.93	0	5.85
I	K	A	A	G	D	2.20	1.33	2.93	0	5.85
I	K	A	A	G	E	2.20	1.33	2.93	0	5.85
I	K	A	A	G	F	2.20	1.33	2.93	0	5.85
I	K	A	A	R	G	2.20	1.33	2.93	1	2.93
I	K	A	A	G	H	2.20	1.57	3.45	1	3.45
I	K	A	A	G	J	2.20	1.33	2.93	0	5.85
I	K	A	A	G	K	2.20	1.33	2.93	1	2.93
I	K	A	A	R	A	2.20	1.57	3.45	0	5.85
I	K	A	A	R	B	2.20	1.57	3.45	0	6.91
I	K	A	A	R	C	2.20	1.57	3.45	1	3.45
I	K	A	A	R	D	2.20	1.57	3.45	0	6.91
I	K	A	A	R	E	2.20	1.57	3.45	1	3.45
I	K	A	A	R	F	2.20	1.57	3.45	2	1.73
I	K	A	A	R	G	2.20	1.57	3.45	1	3.45
I	K	A	A	R	H	2.20	1.57	3.45	0	6.91
I	K	A	A	R	I	2.20	1.57	3.45	1	3.45
I	K	A	A	R	K	2.20	1.57	3.45	0	6.91
I	K	A	A	R	A	2.20	2.20	4.84	0	9.68
I	K	A	A	R	B	2.20	2.20	4.84	0	9.68
I	K	A	A	R	C	2.20	2.20	4.84	0	9.68
I	K	A	A	R	D	2.20	2.20	4.84	0	9.68
I	K	A	A	R	E	2.20	2.20	4.84	0	9.68
I	K	A	A	R	F	2.20	1.57	3.45	1	3.45
I	K	A	A	R	G	1.80	1.33	2.39	0	4.79
I	K	A	A	R	H	2.20	1.57	3.45	0	6.91
I	K	A	A	R	I	2.20	2.20	4.84	1	4.84
I	K	A	A	R	J	2.20	1.57	3.45	0	6.91

Junctional Analyzer took 142.77 seconds.

FIGURE 13D

Figure 3a: CTL responses induced by EP HIV-1090 relative to individual peptides in IFA

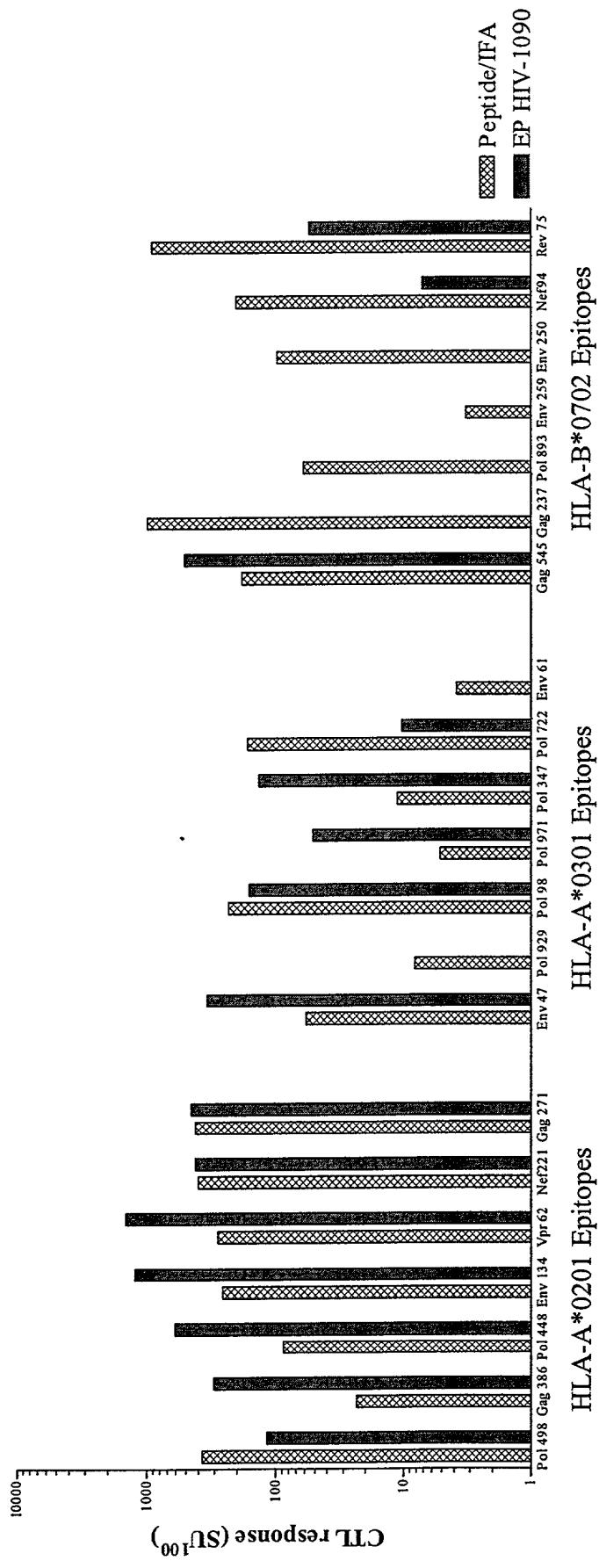
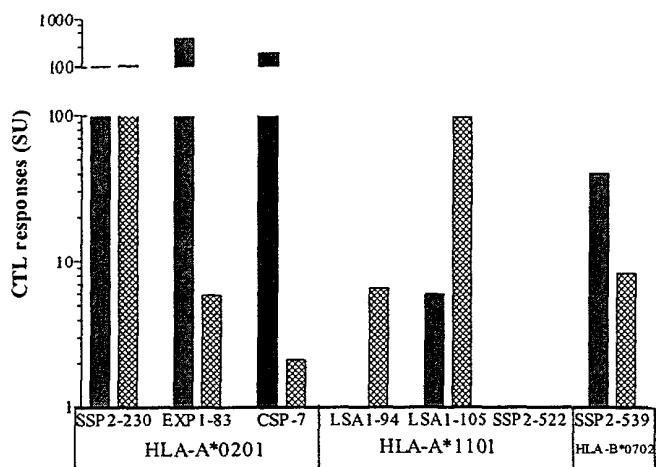
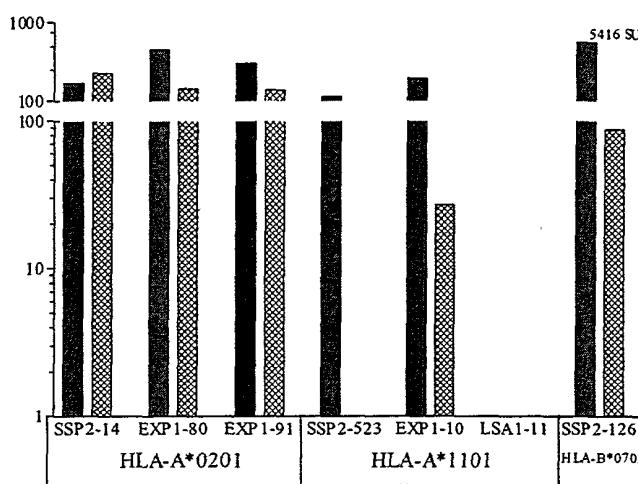


FIGURE 14A

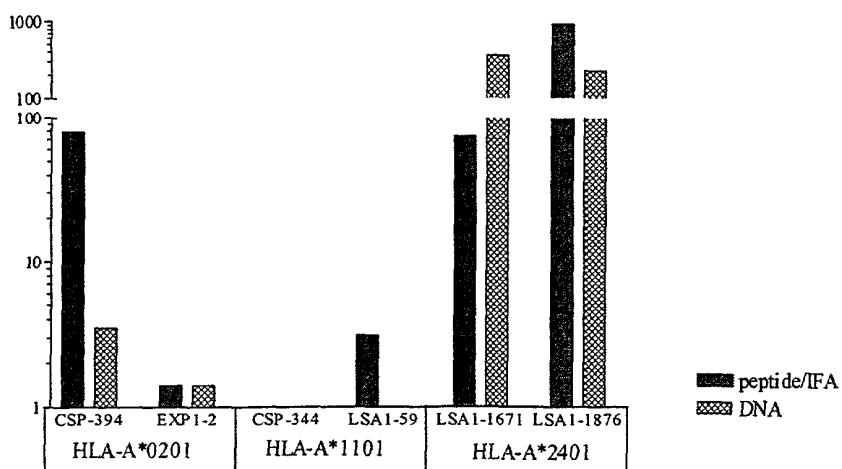
Responses to PfCTL 1



Responses to PfCTL 2



Responses to PfCTL 3



■ peptide/IFA
▨ DNA

FIGURE 14B

FIGURE 15

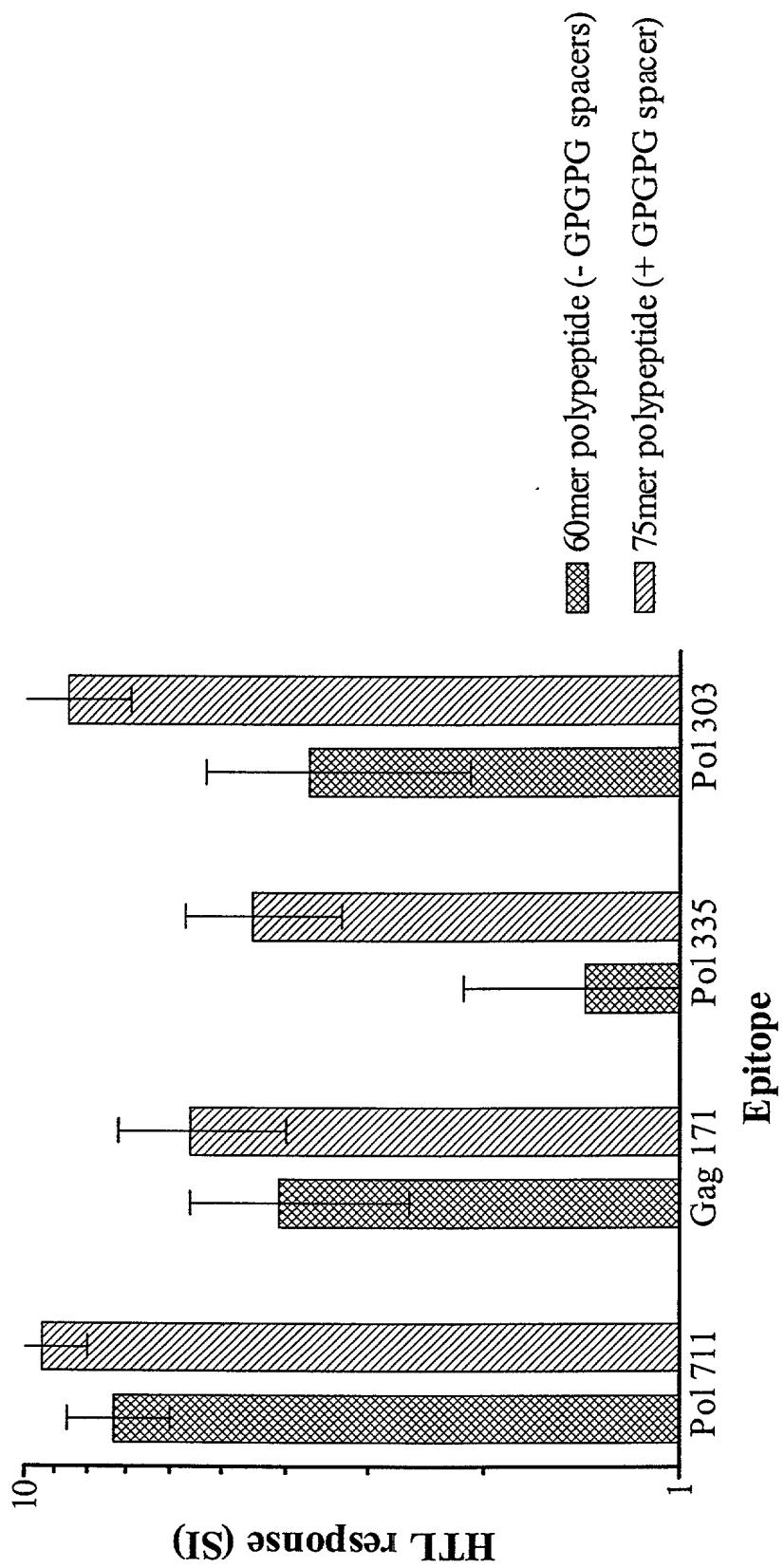


FIGURE 16

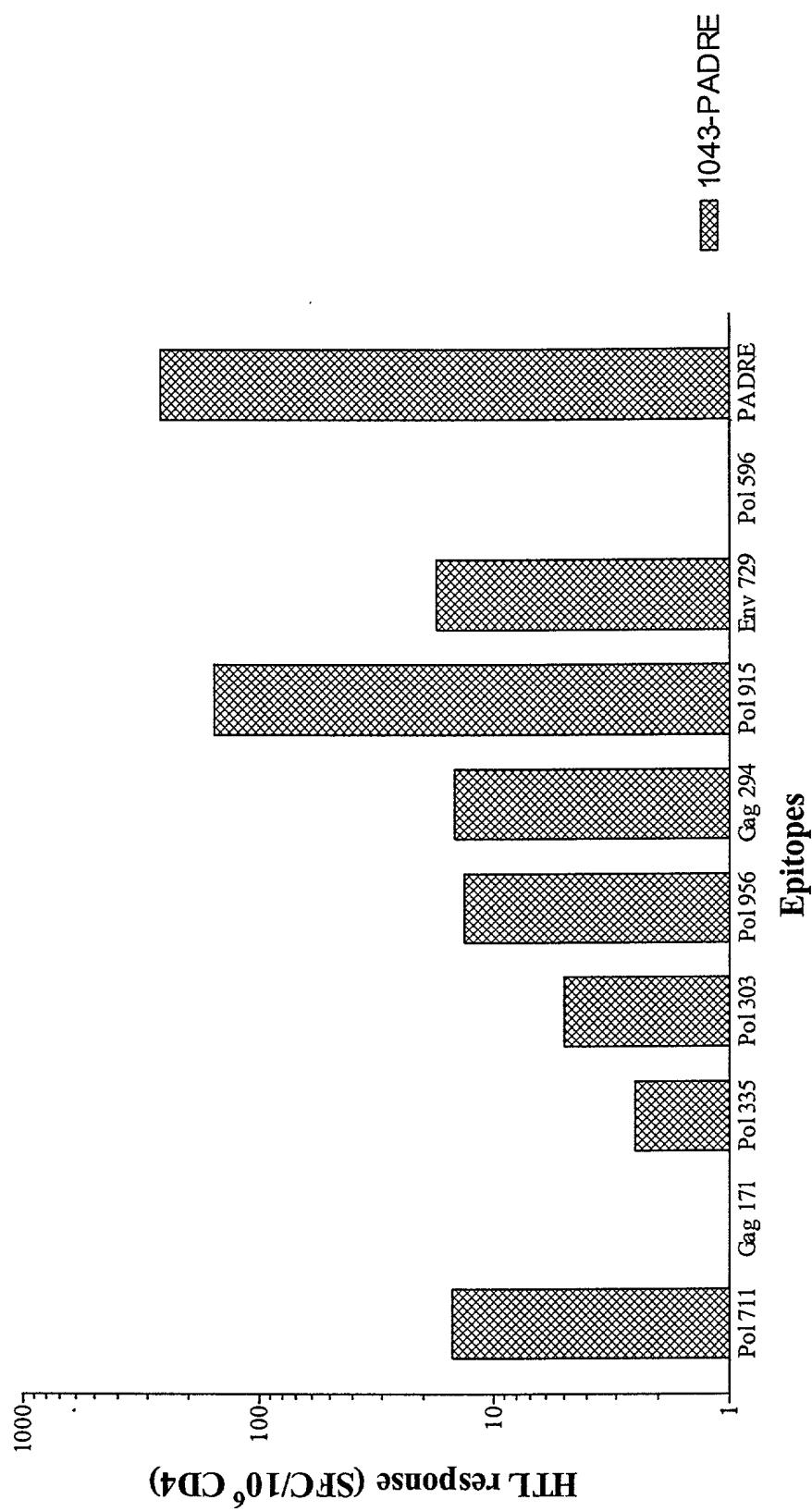


FIGURE 17

HIV 75mer		EP HIV-1043		EP HIV-1043	
Pol 711	GPGPG	Gag 171	GPGPG	Pol 956	GPGPG
711/712	GPGPG	Pol 335	GPGPG	Pol 596	GPGPG
		Pol 303		Vpu 31	GPGPG
				Env 729	GPGPG
				Gag 171	GPGPG
				294/298	GPGPG
				Env 566	GPGPG
				Gag 171	GPGPG
				294/298	GPGPG
				Pol 874	GPGPG
				Pol 915	GPGPG
				Pol 674	GPGPG
				Pol 758	GPGPG
				Pol 619	GPGPG
				Pol 989	GPGPG
				Pol 303	GPGPG
				PADRE	

EP-HIV-1090

MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPVSFEPIKIPHYCAPA
KAKFVAAWTLKAAAKAFPVRPQVPLGAALKTPLCVTLGAAAALAEAMSQVKVYLAWVPAHKG
AAAAIFQSSMTKKTTLFCASDAKNIPYNPQSQGVVKHPVHAGPIANVTVYYGVPVWKAAAQMA
VFIHNFKAAAAYPLASLRSLFNLTFGWCFKLNRLQQLFINAKIQNFRVYYRKAATIKIGGQLKK
VPLQLPPLKAMTNPPIPV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAAAGCTGGTGGGCAAACCTCAACTGGGCCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGG
GGTGAATGCCGCTTGCCCTAAAGTCAGCTCGAACCAATTAAAGATCCCCATTCAATTACTGTGC
ACCTGCCAAAGCTAAGTTGTGGCCGCTGGACCCCTAACGGCCGCTGCAAAGCCTTCCCAGT
GAGGCCCGAGGTGCTCTGGCGCCGCTAAACACTCACACCAGTGCCTGACTCTGGAGCCGC
TGCAGTGTGGCAGAGGCCATGTCCAAGTGAAGGTGTATCTGGCTTGGGTGCCCGCCACAA
GGGGGCCGCTGCAGCCATCTTCAGTCAGTGCATGACCAAGAAAACAACCTGTGTTCTGTGCCTC
CGACGCTAAGAACATCCCATAATCCACAGTCAGGGCGTGGTCAGCATCCCCTGCACGC
CGGACCTATTGCTAACGTGACCGTGTACTATGGGGTCCCAGTGTGGAAGAAAGCCGCTGCACA
GATGGCCGTGTTATTACAATTCAAAAACGCCGCTGCATACCCCTGCCAGCCTGAGATC
CCTCTCAACCTGACATTGGCTGGTGTAAAGCTGAACCGGATCCTGCAGCAACTGCTCTT
ATCAATGCTAAAATCCAGAACCTCCGCGTCTACTATAGGAAGGCTGCAGTGAATGACTATCAAAATT
GGCGGACAACCTGAAGAAAGTGCCTCTCAGCTGCCCTCTCAAGGCAATGACCAACAATCC
CCCTATCCCAGTGTGA

HIV-CPT

MGMQVQIQSLFLLLLWVPGSRGIPHYCAPAKAAKIQNFRVYYRKAATIKIGGQLKKAKFVAAW
TLKAAAKVPLQLPPLKAIFQSSMTKKLTPLCVTLGAQMAVFIIHNFKGAKVYLAWVPAHKNAPIYN
PQSQGVVKAILKEPVHGVAAALTFGWCFKLNALAEAMSQVNRLQQLFINAAACPVSFEPI
KVTVYYGVPVWKAAAHPVHAGPIANAAAYPLASLRSLFNAAATLFCASDAKNKLVGKLNWAN
AAAFPVRPQVPLNMTNNPPIPV

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAATCCCCATTCACTACTGCGCCCTGCTAACGGCAGCCAAATCCAGAACCTCAGGGTGTAT
TACAGAAAGGCTGCAGTCACCATTAAATCGGCGGACAACACTGAAGAAAGCCAAGTTGTGGC
CGCTTGGACACTCAAGGCCGCTGCAAAGGTCCCAGTGCAGCTCCCCCTCTGAAGGCCATCTT
CCAGAGCTCCATGACTAAGAAACTGACCCCAGTGTGTGACACTCGGGGCCAGATGGCTGT
GTTCATCCATAATTAAAGGCCAAGGTCTACCTGGCTGGGTGCCGCACACAAGAACGC
CATTCCTACAATCCACAGTCTCAAGGAGTGGTCAAAGCTATTCTGAAGGAGCCGTGCACGG
GGTGGGCGCCGCTGCACTCACTTCGGATGGTGTAAACTGAACGCCGTGCTGGCTGAAGC
CATGAGCCAGGTCAATCGGATCCTGCAGCAACTGCTCTTCATTAACGCCGCTGCATGTCTAA
GGTGTCTTCAGCCAATCAAAGTGACCGTGTATTACGGGGTCCCCGTGTTGAAGAAAGCCGC
TCATCCTGTCCACGCAGGCCAATGCCAACGCCGCTGCATATCCCTGCCCTCTGCGCAG
CCTGTTAACGCCGCTGCAACAAACCCCTTTGCGCCTCCGACGCTAAGAATAAAACTGGTGGG
AAAGCTGAACGGCCAACGCCAGCTGCATTCCCTGTGAGGCCACAGGTCCCCCTCAATATGAC
TAACAATCCCCCTATCCCAGTGTGA

FIGURE 18A

HIV-FT

MQVQIQSLLLLLWVPGSRGKLVGKLNWAMASDFNLPPVAIFQSSMTKVTIKIGGQLKRILQQLLF
IMAVFIHNFKIPYNPQSQGVVTLFCASDAKILKEPVHGQMAVFIHNFKGAAVFIHNFKRCPKVSF
EPIKIQNFRVYYRLTFGWCFLQVPLRPMTYKMTNNPIPVTVYYGVPVWKVLAEAMSQVIPHY
CAPAKLTPLCVTL

ATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCTGTGGGTGCCCGGATCCAGAGGAAAG
CTGGTGGGAAGCTGAACCTGGCCATGGCCAGCGATTCAACCTGCCCGGTGCCATCTTC
CAGAGCAGCATGACCAAGGTGACCATCAAGATCGGGGGCAGCTGAAGAGGATCCTGCAGCA
GCTGCTGTTCATCATGGCGTGTTCATCCACAACCTCAAGATCCCCTACAACCCCCAGAGCCA
GGGGGTGGTGACCACCCCTGTTCTGCGCCAGCGATGCCAAGATCCTGAAGGAGCCCGTGCACG
GGGTGCAGATGGCCGTGTTCATCCACAACCTCAAGGGCGCCGTGTTCATCCACAACCTCA
AGAGGTGCCCAAGGTGAGCTTCGAGCCCATCAAGATCCAGAACTTCAGGGTGTACTACAGG
CTGACCTCGGGTGGTGCTCAAGCTGCAGGTGCCCTGAGGCCATGACCTACAAGATGACC
AACAAACCCCCCATCCCCGTGACCGTGTACTACGGGGTGCCGTGGAAGGTGCTGCCGAG
GCCATGAGCCAGGTGATCCCCATCCACTACTGCAGCCCCGCCAAGCTGACCCCCCTGCGTG
ACCTG

FIGURE 18B

HIV-TC

MGMQVQIQSLFLLLLWVPGSRGYWQATWIPEWKAIFQSSMTKKVYLAWVPAHKNAACPVSFE-
PIKHPVHAGPIANLTGWCFLNKMIGGIGGFIKFRDYVDRFYKAAARILQQLLINTTLFCASDAK
NQMVKHQAIISPRGAKLVGKLNWAGAAIYETYGDTWKAAQVPLRPMTYKGAAAVTVDVGDAY
NAAARYLKDQQLNLTNFPISPINMTNNPPIPVNAPYNTPVFAIKAAAVPLQLPPLKAAIPYNPQSQ
GVVKALLQLTVWGIGAAILKEPVHGVAACAFPIETVKVWKEATTLFKAAAVTIKIGGQLKKI
YQEPFKNLKAAAVLAEAMSQNVNLGVPTPVNIGAAAEVNIVTDSQYKAAIPIHYCAPAKAVIYQY
MDDLYKAAAQMAVFIHNFKNAATYQIYQEPFKPYNEWTLELAKAKIQNFRVYYRKAFPVRPQVPL
GAAAIWGCSGKLIKVMIVWQVDRNAAKAACWWAGIKAKFVAAWTLKAAAKLPLCVTLNAAM
ASDFNLPPVKSLLNATDIAVNVTVYYGPVWKAAAIIRLQQLKRAMASDFNLNAAAYPLASL
RSLF

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCCGATCTAGA
GGATACTGGCAAGCTACTTGGATTCCAGAACAGCTATCTTCATCCTCAATGACGAAG
AAGGTATAACCTGGCATGGTCCCAGCACACAAGAACGCCGCTTGCCAAAGGTGTCCCTTGAA
CCCATTAACACCCAGTCACGCAGGCCAATAGCGAATTGACATTGGGGTGTGCTTCAAA
CTAAACAAAATGATCGCGGGATTGGAGGTTATCAAGTTAGAGATTACGTGGACCGATTC
TATAAAGCCGCTGCCGTATACTCCAGCAGCTACTATTCAACACACTCTCTCGCGCTT
CAGACGCTAAGAACCAAATGGTACACCAAGCCATAAGCCCTAGAGGAGCCAAGCTCGTAGGG
AAATTAAATTGGGCGGGTGCAGCAGCAATCTACGAGACTACGGCGATACTGGAAAGCAGC
CCAGGTTCCGTTACGCCAATGACCTATAAAGGCAGCAGCAGTAACAGTTAGATGTAGG
AGACGCTTACAACCGTGCAGAAGATACTAAAGATCAGCAGTTACTCAACACACTAAATT
CCCAATTAGCCGATAAACATGACAATAACCCACAATTCCGCTCAATGCTCCCTACAACAC
TCCAGTATTGCAATCAAAGCCGCTGCTGTCCCCCTGCAAGCTCCCTCTGAAAGCTGCGAT
ACCTTACAACCCACAGAGCCAAGGTGTTGTCAAAGCACTGCTTCACTAACAGTTGGGAAT
TGGTGTGCAATTCTAAAAGAGCCAGTTACGGGTTAACGCCGCCCTCCCAATCAGTCC
TATTGAGACTGTGAAAGTATGGAAAGAAGCCACAACCACACTTTTAAGGCAGCCGAGTTA
CAATTAAAATAGGGGCCAACTTAAGAAAATATACCAGGAACCTTCAAGAATCTAAAGCC
GCTGCAGTGTGCTGCCAGGGCTATGTACAGGTGAATTGGTCGGACCAACACCGTAAACATC
GGAGCCGAGCCGAAGTGAACATAGTCACCGACTCACAGTACAAAGCCGCTGCAATACCCAT
ACATTATTGTGCTCCGAAAGGCCGTGATCTATCAATATATGGACGACCTGTATAAGGCC
CGCGCAGATGGCAGTCTTATCCACAACCTTAAAACGCAGCTACTTATCAGATCTACAGGA
ACCATTCAAACCGTACAATGAGTGGACCTTGGAACTAAAGGCCAAATTCAAGACTTCAGGG
TATATTATAGAAAAGCATTCCAGTGAGGCCAGGTGCCTCTGGGTGCCAGCAATATGGG
GATGTTCTGGAAAAGTCAAGGTGATGATTGTATGGCAAGTGGACAGAAATGCAGCTAAG
GCAGCCTGTTGGTGGCAGGTATAAAAGCAAAGTTCTGGCAGCATGGACGCTTAAAGCAGC
CGCAAAACTCACTCCTCTGCGTGACACTTAATGCAGCCATGGCCTCTGATTCAACCTCCC
CCTGTAATCCCTGCTTAATGCGACAGATATCGCAGTCACGTAACAGTATATTATGGCGTG
CCAGTCTGGAAAAAGCCGCCGGCCATAATTGGGAACTTCAGCAGCTGAAAAGAGCTAT
GGCAGGTGACTTCAACCTGAATGCGGCCGCTACCCCTGGCATCGTTAAAGTCACTATTTG
A

FIGURE 18C

HCV.1

MGMQVQIQSLFLLLLWVPGSRGLFNILGGWVDLMGYIPLVYLVAYQATVILAGYAGVRLIVFP
DLGVHMWNFISGIYLLPRRGPRLYLVTRHADVVLVGGVLAALLFLLADAFLLADARVWMNRL
IAFACTCGSSDLYLSAFLSHSYGVAGALVAFKLPGCSFSIFKTSERSQPRLFCHSKKKFWAKHMW
NFIPFYGKAIRMYVGGVEHRQLFTFSPRRLGVRATRKVGIYLLPNRAKFVAAWTLKAAA*

GAATTGCCGCCACCATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCGGATCCAGAGGACTGC
TGTCAACATCCTGGGGGGTGGATCTGATGGGTACATCCCCCTGGTGTACCTGGTGGCCTACCAGGCCACCGT
GATCCTGGGGGGTACGGGCGGGGTGAGGCTGATCGTGTTCGGATCTGGGTGACATGTGGAACCTTCATCAGC
GGGATCTACCTGCTGCCAGGAGAGGACCTAGACTGTACCTGGTACTAGACACGCTGATGTGGTGTGGGAGGAG
TGCTGGCTGCTCTGCTGTTCTGCTGCTGGCTGATGCTTCTGCTGGTGTGGGAGGAG
GATCGCTTCGCTTGTACATGTGGAAGCTCCGATCTGTATCTGAGCGCTTCAGCCTGACAGCTACGGAGTGGCTGGA
GCTCTGGTGGTTTAAGCTGCCTGGATGTAGCTTAGCATCTTAAGACAGCGAAAGAAGCCAGCCTAGACTGATCT
TTTGTCAACAGAAGAAGTTGGCTAACGACATGTGGAATTATCCTTCTATGGAAAGGCTATCAGAATGTA
TGTGGGAGGAGTGGAACACAGACAGCTGTTACATTAGCCCTAGAAGGAGACTGGGAGTGGAGAGCTACAAGAAAGGTG
GGAATCTATCTGCTGCCAACAGATGAAAGCTTGGG*

HCV.2

MGMQVQIQSLFLLLLWVPGSRGLMGYIPLVAKFVAAWTLKAAALLFLLADALIFCHSKKKQLF
TFSPRRYLVTRHADVYLLPRRGPRLCGSSDLYHMWNFISGIFWAKHMWNFAKFVAAWTLKAA
AILAGYAGGVYLVAYQATVGVAGALVAFKIPFYGKAIRMYVGGVEHRVLVGGVLAFLADA
RVLPGCSFSIFAKFVAAWTLKAAAKTSERSQPRRLGVRATRKRLIVFPDLGVWMNRLIAFALSAFS
LHSYLLFNILGGWVVGIVYLLPNR*

GAATTGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGATCTGATGGGATATATCCTCTGGCTAAGTTGTGGCTG
TGGACACTGAAGGCTGCTGCTGCTGTTCTGCTGGCTGATGCTCTGATCTTCTGTCACA
GCAAGAAGAAGCAGCTGTTACATTAGCCAAGAAGATATCTGGTACAAGACACGCTGAT
GTGTATCTGCTGCCTAGACCGCGGACCTAGACTGTGTACATGTGGAAGCTCCGATCTGTATCAC
ATGTGGAACCTTATCAGCGGAATCTTGGCTAAGCACATGTGGAATTCTATCCTGGCTGGA
TATGGAGCTGGAGTGTATCTGGTGGCTTACAGGCTACAGTGGAGTGGCTGGAGCTGGT
GCTTCAAGATCCCATTCTATGGAAAGGCTATCAGAAATGTATGTGGGAGGAGTGGAAACACAG
AGTGTGGTGGAGGAGTGTGGCTGCTGCTGCTGGCTGATGCTAGAGTGTGCTGCCAGG
ATGTAGCTTACATCTCAAGACTTCCGAACGCTCCAGCCTAGAAGACTGGGAGTGGAGAGC
TACAAGGAAGAGACTGATCGTGTTCAGATCTGGGAGTGTGGATGAATAGACTGATCGCTT
CGCTCTGAGCGCTTCAGCTGCACAGCTATCTGCTGTTCAACATCCTGGAGGATGGGTGG
GGAATCTATCTGCTGCCAACAGATGAAAGCTT

HCV.3s1

MGMQVQIQSLFLLLLWVPGSRGLVAYQATVAKFVAAWTLKAAALLFLLADALIFCHSKKKYL
VTRHADVLGFAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNF*

GAATTGCCGCCACCATGGGAATGCAGGTGCAGATCCAAGCCTGTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGATACTCGTCGCCCTACCAAGGCCACTGTGGCTAAATTCTGTCAGCC
TGGACACTGAAAGCTGCAGCTGCTCTGCTCTCTGCTGGCCATGCACTCATCTGCCATT
CCAAGAAAAAGTATCTGGTCAACAGACATGCTGACGTGCTGGGGTTGGCGCCTACATGAGC
AAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACCTTATTCATGGAATCTTGGG
CCAAGCACATGTGGAATTCTGAAAGCTT

FIGURE 18D

HCV.3s2

MGMQVQIQSLFLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLADARVLSAFSLHSYIL-
AGYGAGVWMNR利亚FAIPFYKAIVAGALVAFKVGIVYLLPNR*

GAATTGCCGCCACCATGGGAATGCAGGTGCAGATCCAAGCCTGTTCTGCTCCTCTGTGG
GTGCCCGGATCCAGAGGGACTCCTGGTGGCGCGCTCTGCCGCTGCTAAGTTGTCGCTGCT
TGGACACTGAAGGCAGCCGCTTCCTGCTCCTGCCAGACGCCAGGGTGTCTGCCCTCAGC
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCCTGGATGAATCGGCTGATGCCCTT
GCCATTCCATTCTATGGGAAAGCCATTGTGGCTGGCGCCCTGGCATTCAAGGTCGGGATC
TACCTCCTGCCTAACCGCTGAAAGCTT

HCV.3s2(-3)

MGMQVQIQSLFLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLADARVLSAFSLHSYIL
AGYGAGVWMNR利亚FA*

GAATTGCCGCCACCATGGGAATGCAGGTGCAGATCCAAGCCTGTTCTGCTCCTCTGTGG
GTGCCCGGATCCAGAGGGACTCCTGGTGGCGCGCTCTGCCGCTGCTAAGTTGTCGCTGCT
TGGACACTGAAGGCAGCCGCTTCCTGCTCCTGCCAGACGCCAGGGTGTCTGCCCTCAGC
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCCTGGATGAATCGGCTGATGCCCTT
GCCTGAGGATCC

HCV.3s3

MGMQVQIQSLFLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAARLGVRATRKLLFNILGGWV
RMYVGGVEHRR利VFPDLGVGVAGALVAFKLPGCSFSIFKTSERSPRQLFTFSPPRYYLLPREGPRL

GAATTGCCGCCACCATGGGAATGCAGGTGCAGATCCAAGCCTGTTCTGCTCCTCTGTGG
GTGCCCGGATCCAGAGGGACCTGATGGGCTACATCCCTCTCGTGGCCAAGTTGTCGCTGCT
TGGACCCCTGAAGGCCGCTGCCAGACTGGGAGTGCCTGCGCTACACGAAAACCTCTGTTAACATC
CTGGGAGGGTGGGTGCGGATGTACGTCCGAGGCCTGAGCACAGAAGGCTCATGTCTTCC
AGATCTCGCGTGGCGTCAAGGCCTGGCCTCAAACGTCCAGACAGCTGTTCACTTCTCCTCGGAGGTAT
CTGCTGCCAGACGCCAGGGCTGTGAAAGCTT

HCV.PC3

MGMQVQIQSLFLLLWVPGSRGLFNILGGWVKAKFVAAWTLKAAALADGGCSGGAYRLIVFPD
LGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPPR*

GAATTGCCGCCACCATGGGAATGCAGGTGCAGATCCAAGCCTGTTCTGCTCCTCTGTGG
GTGCCCGGATCCAGAGGGACTGCTCTCAACATCCTGGCGGATGGGTGAAGGCCAAGTCGCTG
GCTGCCCTGGACCCCTGAAGGCTGCCGCTCTGCCAGGGGGATGCAGCGGCGGAGCTTACAG
GCTCATTGTCCTTCCGATCTGGAGTCAAATTGGCAAAGCACATGTGAATTTCATCGG
GGTGGCCGGAGCCCTGGTCGCTTAAAAAGCAGCTTCACTTCTCCCCAAGACGGTGAGG
TACC

FIGURE 18E

HCV.PC4

MGMQVQIQLFLLLWVPGSRGRLGVRATRKAKFVAAWTLKAAAKTSERSQPRNLPGCSFSIFN
DLMGYIPLVKYLLPREGPRLNTLCGFADLMGYRMYVGGVEHR*

GAATTGCCGCCACCATGGGAATGCAGGTGCAGATCCAAGCCTGTTCTGCTCCTCTGTGG
GTGCCCGGATCCAGAGGAAGGCTGGCGTGAGAGCCACCCGGAAGAAGGCCAAGTTCGTGGC
TGCCTGGACCCTGAAGGCTGCCCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTG
GATGCTCTTCAGCATTTAATGACCTCATGGGTACATTCCACTGGTGAAGTATCTGCTCCC
CAGACGGGGCCCTGCCCTGAACACTCTGTGGATTGCTGATCTGATGGGTACAGGATGTA
TGTGGCGGAGTCGAACACAGATGAGGTACC

HCV.243(1P)

MGMQVQIQLFLLLWVPGSRGVLVGGVLAAAFLLADARVLSAFSLHSYILAGYGAGVWMNRL
IAFAGAAARLGVRATRKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVKYLLPREGPRLNTLCG
FADLMGYRMYVGGVEHRKLLFNILGGWVKAALADGGCGGAYRLIVFPDLGVKFHAKHMWN
FIGVAGALVAFKKQLFTSPRRNGYLVAYQATVAAALLFLLADALIFCHSKKYLVTRHADVLG
FGAYMSKCTCGSSDLYHMWNFISGFWAKHMWNKAAAACKVAAWTLKAAA

GAATTGCCGCCACCATGGGAATGCAGGTGCAGATCCAAGCCTGTTCTGCTCCTCTGTGG
GTGCCCGGCTCCAGAGGAGTCTGGTGGCGCGCTGGCAGCCCTTCCCTGCTCCTGGCA
GACGCCAGGGTGTCTGCCTTCAGCCTCACTCCTACATCCTCGCAGGGTATGGCGCAGGC
GTGTGGATGAATCGGCTGATCGCTTGCCTGGCGCTGCCGCAAGGCTGGCGTGAGAGCCACC
CGGAAGAAGGCTGCCCTAAAACAAGCGAGCGCTCCCAGCCAGGAACCTGCCCTGGATGCTC
TTTCAGCATTTAATGACCTCATGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGG
GGCCCTCGCCTGAACACTCTCTGTGGATTGCTGATCTGATGGGTACAGGATGTATGTCGGC
GGAGTCGAACACAGAAAAGTCTCTCAACATCCTGGCGGATGGGTGAAGGCTGCCGCTCT
GGCCGACGGGGATGCAGCGCGGAGCTACAGGCTCATGCTCTTCCGATCTCGGAGTC
ATTGGCAAAGCACATGTGGAATTCTACCTGGGTGGCCGGAGCCCTGGTGCCTTTAAAAAA
GCAGCTCTCACCTCTCCCCAAGACGGAACGGATACTCGTCGCCCTACAGGCCACTGTGGC
TGCAGCTCTGCTCTCTGCTCTGGCGATGCACTCATCTGCTGCCATTCAAGAAAAAGTAT
CTGGTCACCAGACATGCTGACGTGCTGGGTTGGCGCCTACATGAGCAAGTGCACCTGTGGC
AGCTCCGACCTGTATCACATGTGGAACATTCTGGAACTTTATCTGGAACTTTGGCCAAGCACATGTGG
AATTGAAAGGCCGAGCAGCTAAATTGTCAGCAGCTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGG
ATCC

FIGURE 18F

HCV.4312(1P)

MGMQVQIQSLFLLLWVPGSRGLGVRATRKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVK-YLLPRRGPRLNTLCGFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFPDLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPPRNGYLVAYQATVAAALLFLLADALIFCHSKKKYLVTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGFWAKHMWNFKAAAVLVGGVLAAAFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFANAAAKFVAAWTLKAAA*

GAATTGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTCTGCTCCTCCTGTGGTGCAGCTCCCAGGGAGAAGGCTGGCGCTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAACAAAGCGAGCGCTCCCAGGGAGAACCTGCCTGGATGCTCTTCAGCATCTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTGCCCTGAACACTCTGTGGATTGCTGATCTGATGGGTACAGGATGTATGTCGGCGAGTCGAACACAGAAAAGTCTCTCAACATCCTGGCGATGGGTGAAGGCTGCCCTGGCCGACGGGGATGCAGCGCGGAGCTTACAGGCTCATTGCTTCCCAGTCGGAGTCAAATTGGCAAAGCACATGTGGAATTTCATCGGGTGGCCGGAGCCCTGGTCGCTTTAAAAAGCAGCTCTCACCTCTCCCCAA GACGGAACGGATAACCTCGTCGCCTACCAGGCCACTGTGGCTGCAGCTCTGCTCTCCTGCTCC TGGCGATGCACTCATCTCTGCCATTCAAGAAAAAGTATCTGGTACCCAGACATGTCGACGTGCTGGGGTTGGCGCCTACATGAGCAAGTGCAACCTGTGGCAGCTCCGACCTGTATCACATGTTGAACCTTATTCCTGGAATCTTGGCCAAGCACATGTGGAATTAAAGAAAGCCGCTGCAGTCCTGGCGCTCTGGCAGCCAGGGTGTGCTG CTCITCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGGTGTGGATGAATCGGCTGATCGCCTTGCCAATGCTGCAGCTAAATTGTCGGCAGCCTGGACACTGAAAGCAGCTGCATGAGGATCC

AOSI.K

MGMQVQIQSLFLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAFLPSDFPSVKFLSLGIHLYMDDVVLGVGLSRYVARLFLTRLTISTLPETTVVRRQAFTFSPTYKWLSSLVPFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCGGGTCCAGAGGACACACCCCTGTGGAAGGCCGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCCTGAAGGCTGCCGCTTCCCTGCCTAGCGATTCTTCCTAGCGTGAAGTTCTGCTGTCCCTGGAA TCCACCTGTATATGGATGACGTGGTGTGGAGTGGACTGTCCAGGTACGTGGCTAGGCTGTCTGCTGACCAGAACCTGACCATCTCCACCCCTGCCAGAGACCACCGTGGTGAGGAGGCAGGCTTCACCTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCTTGTGTGA

HBV.1

MGMQVQIQSLFLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAFLPSDFPSVFLLSLGIHYMDDVVLGVGLSRYVARLFLTRLTISTLPETTVVRRQAFTFSPTYKWLSSLVPFVIPISSWAFTP ARVTGGVFVGNFTGLYLPSDFFPSVTLWKAGILYKNVSIPWTHKLVVDFSQFSRSAICSVVRAL MPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCGGGTCCAGAGGACACACCCCTGTGGAAGGCCGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCCTGAAGGCTGCCGCTTCCCTGCCTAGCGATTCTTCCTAGCGTGAAGTTCTGCTGTCCCTGGAAATCCACCTGTATATGGATGACGTGGTGTGGAGTGGACTGTCCAGGTACGTGGCTAGGCTGTCTCTGCTGACCAGAACCTGACCATCTCCACCCCTGCCAGAGACCACCGTGGTGAGGAGGCAGGCCTTCACCTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCTTGTGATCCCTATCCCTAGCTCCTGGCTTTCACCCCAAGCCAGGGTGACCGGAGGAGTGTGTTAAAGGTGGAAACTTCACCGGCTGTATCTGCCAGCGATTCTTCCTAGCGTACCCCTGTGGAAAGGCCGGATCCTGTACAA GAATGTGTCCATCCCTGGACCCACAAGCTGGTGGACTTTCCAGTTCACTGAGCAGATCCGCTATCTGCTCCGTGGTGAGGAGAGCTGTGATGCCACTGTATGCCTGTATCTGA

FIGURE 18G

HBV.2

MGMQVQIQSLFLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFPLSDFFPSVNFLSLGIHLYMDDVVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIPSSWAFKTPARVTGGVFVGNTGLYNLPSDFPSVKTLWKAGILYKNVSIPWTHKGAAJVVDFSQFSRNSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCCGGTCCAGA
GGACACACCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTCGTGGCTGCCCTGGACCCCTG
AAGGCTGCCGCTTCTGCCTAGCGATTCTTCCTAGCGTAACTCCTGCTGTCCCTGGAA
TCCACCTGTATATGGATGACGTGGTCTGGGACTGTCCAGGTACGTGGCTAGGCTGT
TCTGCTGACCAGAACCTGACCATCTCCACCCGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTCACCTTAGCCCTACCTATAAGGGAGCCGCTGCCCTGGCTGAGCCTGCTGGTCCCTTGT
GAATATCCCTATCCCTAGCTCCTGGGCTTCAAGACCCCCAGCCAGGGTGACCCGAGGAGTGT
TAAGGTGGAAACTTCACCGCCGTATAACCTGCCAGCGATTCTTCCTAGCGTAAGAC
CCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCATCCCTGGACCCACAAGGGAGCCG
CTCTGGTGGTGGACTTTCCAGTTCAAGCAGAAATTCCGCTATCTGCTCCGTGGTGAGGAGAG
CTCTGATGCCACTGTATGCCCTGTATCTGA

PfCTL.1

MQVQIQSLFLLLWVPGSRGILSVSSFLFVNAAAQTNFKSLLRNLPSENERGYKAAALLACAGLAY
KKAAAAKFVAAWTLKAAAKFMKAVCDEVNAASFLFVEALFNATPYAGEPAPFKAAKYKLA
TSVLKAGVSENIFLKNAAYFILVNLLIKAGLLGVVSTV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCCGATCCAGA
GGAATCCTGAGCGTGTCCCTTCTGTTGTCAACGCCGCTGCACAGACCAATTCAAGAGC
CTCCTGAGGAACCTCCCTCCGAGAACGAAAGAGGGCTACAAAGCCGCTGCACTGCTGCCCTGC
GCTGGACTGGCCTATAAGAAAGCCGCTGCAGCCAAGTCGTGGCCGCTGGACACTGAAGGC
CGCTGCAAAGCCTTATGAAGGCTGTGTGGAGGTCAATGCCGCTGCATCTTCTGT
GTGGAGGCCCTTTAACGCTACTCCTACGCAGGGGAACCAGCCCCCTCAAGGCCGCTGCA
AAATATAAGCTGGCAACCAGCGTGTGAAGGCTGGCGTCCGAGAATATTTCTGAAAAAC
GCCGCTGCATACTCATCCTGGTGAATCTGCTCATTAAGGCCGACTCCTGGGGTGGTCTCT
ACAGTGTGA

PfCTL.2

MQVQIQSLFLLLWVPGSRGFVEALFQEYNAAAKYLIVFLINALACAGLAYKKFYFILVNLLKA
ALFFIIFNKNAAKFVAAWTLKAAAKFILVNLLIFHNFQDEENIGTYKLPYGRNLKAAAVLLGGV
GLVLNFLIFFDLFLVKAVLAGLLGVV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCCGATCCAGA
GGATTCTGGAGGCCCTGTTCAAGGAATACAACGCCGCTGCAAAGTATCTCGTCATCGTGTTC
CTGATCAATGCTCTGGCATGCCGCCCTCGCTTACAAAAAGTTTACTTCATTCTGGTCAACC
TGCTCAAGGCCGCTGTTCTTATCATTTCAATAAAACGCCGCTGCAAAGTTGTGGCCGC
ATGGACCTGAAGGCCGCTGCAAATTCATCCTCGTGAATCTGCTCATTTCAACAATTCCAA
GACGAGGAAAATACCGAATTATAAGCTGCCCTACGGGAGGACAAACCTGAAAGCCGCTGC
AGTCCTGCTCGCGAGTGGGGCTGGTGTCAATTCTGATCTTCTTGATCTGTTCTGGTGA
AAGGCCGCTGGCCGCTGCTGGAGTCGTGTGA

FIGURE 18H

PfCTL.3

MQVQIQSLFLLLLWVPGSRGVFLIFFDLFLNAAAPSDGKCNLYKAAAATCGNGIQRKLHFIFDGD
NEIKAHVLSHNSYEKNEYGKQENWYSLKKILSVFLANAAAKFIKSLFHIFKAAALYISFYFIKAKF
VAAWTLKAAAKAAAYYIPHQSSLKAAAGLIMVLSFL

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCTGTGGGTGCCGGATCCAGA
GGAGTGTTCTGATCTTCTTGACCTGTCCTGAACGCCGTCACCCAGCGATGGCAAGTGC
AATCTCTACAAGGCCGTCAGTGACCTGTGGAAACGGGATTAGTCAGGAAACTCTTCAC
ATCTCGACGGCGATAACGAGATCAAGGCCATGTGCTGCCCACAATTCTATGAAAAAAAC
TACTATGGAAAGCAAGAGAATTGGTACAGCCTGAAGAAAATTCTGTCCGTGTTCTCGCC
AACGCCGCTGCAAAGTTATCAAGTCTGTTCCATATTCAAGGCCGTCACACTACATCA
GCTTCTATTATTAAAGCAAATTGTGGCCGCTGGACACTGAAGGCCGTCGAAAGGCCG
CTGCATACTATATCCCTCACCAAGAGCTCCCTGAAGGCCGTCAGGGCTGATCATGGTGCTCT
CTTCCTGTGA

PfCTL/HTL(N)

MQVQIQSLFLLLLWVPGSRGVNFVNNSIGLIMVLSFLGPGLYISFYFILVNLLIFHINGKIIKN
SEGPGPGPDSIQDSLKESRKLSPGPGLVLAGLLGVSTVLLGGVGLVLPGPGLPSENERGYYIPHQ
SSLGPGPGQTNFKSLLRNLGVSENIFLKGPGPQFQDEENIGIYGPGPGLYKLVIVFLIFFDLFLVPGP
GKFIKSLFHIFDGDNIEGPGPDKSKYKLATSVLAGLLGPGLPYGKTNLGPGRHNWVNHA
AMKLIGPGPGMRKLAISVSSFLVEALFQEYGPGPVGTCNGIQRVGPGLPMNYYGKQENWYSL
KKGPGPGLSDGKCNLYADSAWENVKNIGPFMKA
VCVEVGPGPKILSVFFLAFFIIFNKGPGPG
HVLSHNSYEKGPGPDKYKIAGGIAGGLALLACAGLAYKFVVPGAATPYAGEPAPF

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCTGTGGGTGCCGGATCCAGA
GGAAGTAGTGTGTTCAATGTTGAACCATCAATTGGTCTGATCATGGTCTGAGCTTCTCG
GGCCAGGGCCAGGATTATATATTCTTCACTTCATCCTGTCACCTGTTAATATTCCACAT
TAACGGAAAATAAAAGAACAGTGAAGGCCCTGGGCTGGGCTGACTCGATCCAGGATT
CTCTAAAAGAATCGAGGAAGCTCTCCGGACCAGGCCCTGGTGTACTCGCCGGTTGCTGGGA
GTAGTTAGCACAGTGTGTTAGGAGGGCTCGCTTAGGACCTGGACCAGGTCTGCCG
TCCGAAAACGAAAGAGGATACTACATACCTCACCAAGAGCAGCCTCGGCCAGGCCCGGACA
AACCAATTCAAATCCCTCTTGC
AAATCTAGGAGT GAGCGAGAACATATTCTAAAGGACC
CGTCCCGCTTCAAGGACGAGGAGAATATAGGTATTACGGTCCAGGACCTGGAAAATACCT
AGTATCGTATTCTTAATTITGACCTATTCTGGTGGGCCAGGTCCCAGGAAAGTCATT
AAATCACTCTTCCACATTITGACGGAGATAACGAGATAGGACCCGGTCCCAGGAAATCAA
GTACAAACTAGCCACTTCAGTGCTGGCCGGCTCTAGGCCGGGCCAGGGCTCCCATTGG
AAAGACAAATCTTGGCCCGTCCAGGACGGCACAACGGTGAATCATGGITCCATTGG
CCATGAAACTAATCGGGCCCGTCCAGGCATGCGAAACTGCAATTCAAGCGTAAGITCAT
TTCTGTTCTAGAGGCAGTGTTCAGAAATATGCCAGGACCTGGCTCACATGTGGAAATG
GGATCCAGGTGAGAGGACCGGGACCTGGTATGAACATTACGGTAAACAGGAAAATTGGTAC
TCCCTGAAAAGGGTCCAGGCCCGGCCCTCAGATGGTAAGTGCACCTGTATGCTGACTCA
GCATGGGAGAACGTAaaaaAAATGTAATAGGCCATTGATGAAGGCAGTTGTGTCGAAGTCGG
ACCAGGCCAGGAAAATACTTCTGTTCTCCTAGCTCTTCTCATCATCTCAACAAG
GGACCAGGCCAGGTACGTGTTATCCATAACTCTTATGAAAAGGGCCAGGACCTGGAA
ATACAAAATCGCAGGAGGGATGCCGGGGTAGCGCTCCTGCCTGCGCAGGCTGGCTTA
CAAATTCTGTACCAGGAGCTGCAACACCCATTGCAAGGAGAACCTGCCCAATTGAAGATC
TGC

FIGURE 18I

Pf33

MGMQVQIQSLFLLLLWVPGSRGMKAVCVEVNVTGNGIQVRKGLIMVLSFLNAALFHIFDGDN
EIKAALLACAGLAYKKSFLVEAFLNAAPSDGKCNLYKAAQTNFKSLRNLPSENERGYKAAGVS
ENIFLKNAAYFILVNLLIKAAAILSVSSFLFVNTPYAGEPAPFKAAAKYKLATSVLKAAVFLIFFDL
FLNYYIPHQSSLKAAGLLGVSTVGAVLLGGVGLVNLACAGLAYKAKFIKSLFHIFKAAFYFIL
VNLLKAFLIFFDLFLVKALFFIIFNKNYYGQENWYSLKVEALFQEYNAAAKFVAAWTLKAAAK
ILSVFFLANAVLAGLLGVNFQDEENIGIYKAAALYISFYFIKAFILVNLLIFHNAALPYGRTNLKAA
HVLSHNSYEKNAAKYLVIVFLI

GCCGCCACCAGGGAAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCTGTGGGTGCC
GGATCCAGAGGATTATGAAAGCTGTCGTGTAGAGGTGAATGTAACATGCGGTAAACGGAAT
TCAGGTGAGAAAGGGACTCATGTTACTCAGCTTCTGAACGCAGCCCTGTCACATCTT
TGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCCGGACTAGCCTATAAAAAGA
GTTTCCTTTCGTTGAAGCACTATTAAACGCAGCACCCAGTGACGGTAAATGCAACCTATATA
AACGAGCTCAGACTAATTCAAAGCCTGTTAAGAAATCTGCCCTCAGAGAATGAAAGGGT
TACAAAGCCGCCGGCGTGTCCGAGAATATTTCTGAAGAACGCCGCTGCTTATTTACTC
GTGAATCTACTCATAAAGGCAGCCGCAATCCTTCAGTGCCAGCTTCTGTTAACACAC
CATATGCGGGCGAGCCGGCTCTTCAAGGCTGCAGCAAAATACAAGCTTGCACATCAGTAT
TGAAAGCAGCTGTTTGTATTCTTGTATTCTTAAACTACTACATACTCATCAGTCT
AGTCTTAAAGCAGCCGGCTACTGGGAACGCTCTACTGTTGGGGCCGCTTACTGGAGGA
GTTGGCCTCGTGTGAACCTCGCGTGCAGGCTGTCCTACAAAAAAGCGAAATTCAAG
TCTCTGTTCCACATTAAAGCCGCATTCTATTCTACTAGTGAAACCTCTCAAAGCTTCC
GATCTTCTCGATCTATTCTCGTAAAGCGCTATTCTCATTATCTTAAACAAAAATTATTAC
GGCAAGCAAGAAAATTGGTACTCACTCAAGTTGTTAGAAGCTCTGTTCCAGGAATACAACGCC
GCTGCTAAATTGTTGAGCTTGACCTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTC
TCGCTAATGCCGTATTAGCAGGACTCTAGGCAACGTGAACCTCAAGACGAAGAGAATATAG
GCATCTACAAAGCCGAGCACTGTACATTCTACTCTCATCAAGGCCTTACTGGTCAA
CCTTCTGATATTCTATAATGCAGCACTGCCATAGGGAGAACCAACTGAAAGCGGCCACGT
GTTGAGCCACAACCTCTACGAGAAGAACGCCGCCGAAATATCTCGTCTTCTGAT
TTGA

TB.1

MQVQIQSLFLLLLWVPGSRGRMSRVTTFTVKALVLLMLPVVNLMIGTAAAVVKALVLLMLPVGA
GLMTAVLVGAAAMALLRLPVKRMFAANLGVNLSYFGGICVGRPLVLPNAVAAAACKVAAWT
LKAAAKAAARLMIGTAAAGFVVALIPLVNAMTYAAPLFVGAAAAMALLRLPLV

ATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCTGTGGGTGCCGGATCCAGAGGAAGG
ATGAGCAGAGTGACCACATTCACTGTCAAGGCCCTGGTGTCTGATGCTCCCCGTGTAAC
CTGATGATCGGCACCGCTGCAGCGTCGTGAAAGCTCTGTCCTGCTCATGCTCCCTGTGGGA
GCAGGGCTGATGACAGCGTGTACCTGGTGGCGCTGCAGCCATGGCCCTCTGCCGCTGCCA
GTGAAGCGCATGTTGCTGCAAATCTGGGAGTCAACTCCCTCTATTGCGGGCATTGCGTG
GGAAGGCTGCCCTCGTGTGCTGTCGTGAAATGCAAGACTGATCGGACCGCCGCTGCCGGCTT
ACTCTGAAGGCAGCCGTAAGGCCGCTGCAAGACTGATCGGACCGCCGCTGCCGGCTT
CGTGGTCGCCCTGATTCCCCTGGTGAACGCCATGACATACGCAGCTCCTGTGTTGTGGAGC
CGCTGCAGCCATGGCTCTCCTGCCGCTGCCACTGGTGTGA

FIGURE 18J

BCL A2 #90

MQVQIQSLFLLLWVPGSRGIMIGHLVGVNRLQETELVNAKVAEIVHFLNAKVFGSLAFVNAYL-SGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGRVNAAAATVGIMIGVNAKLCPVQLWV

ATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAATT
ATGATCGGCCATCTGGTGGCGTCACAGACTGTCAGGAAACCGAGCTGGTGAATGCCAA
GGTGGCCGAAATTGTGCACTTCTAACGCAAAGGTGTTGGTCCCTGGCTTTGTCAATGCC
TATCTGAGCGCGCTAACCTAACGTCGGAGCCGCTACCTCCAGCTGGTCTCGGCATCGAG
GTCAACGCTGCTGAAAATTCTGTCAGCTGGACCCCTAACGGCTGCAGCAAAGGCTGCCGCC
GTCGTGCTCGGAGTGGTGTGGGATCAACTATGCCACCTCCCAGGACTAGGGTCAATGCT
GCCGCCAACAGTGGAAATCATGATTGGGTGAATGCCAAACTGTGCCAGTGCAACTGTG
GGTGTGA

BCL A2 #88

MQVQIQSLFLLLWVPGSRGVVLGVVFGINAAAASFVAAWTLKAAAKVAEIVHFLNAYLSANLNVGAAYLQLVFGIEVNIMIGHLVGVNRLQETELVNAKVFGLAFVNNAKLCPVQLWVNAAAATVGIMIGVNSMPPPGRV

ATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAGTC
GTGCTGGGAGTCGTCTCGGCATTAATGCCGCCGTGCAAAGTTCGTGGCTGCCCTGGACCCCTG
AAGGCCGAGCTAAAGTGGCAGAGATCGTCACTTCTAACGCCTACCTGAGCGGAGCAA
TCTGAACGTCGGCGCTGCCTATCTGCACTCGTGTGGATTGAAGTGAACATCATGATTGG
ACATCTGGTGGCGTGAACAGGCTGCTCCAGGAAACTGAGCTGGTCAACGCTAAAGTGTG
GGTCTCTCGCCTTGTAACGCTAACGCTCTGCCCGTCCAACCTGGGTCAATGCCGCAGCCG
CTACAGTGGGATCATGATCGCGTGAACCTCCATGCCCTCACCAAGGGACCAGAGTGTGA

BCL A2 #63

MQVQIQSLFLLLWVPGSRGKLCPVQLWVNAAAATVGIMIGVNIIMIGHLVGVNRLQETELVNAKVAEIVHFLNAKVFGSLAFVNAYLSANLNVGAAYLQLVFGIEVNAAASFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGRV

ATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAAAG
CTCTGCCCCGTGCAACTGTGGGTCAACGCCGCCGCAACCGTCGGCATTATGATCGGGGTG
AACATCATGATCGGACACCTGGTCGGCGTGAACAGGCTGTCAGGAGACAGAACTGGTCAA
TGCCAAGGTGGCTGAAATTGTCCTTCTGAATGCCAAAGTGTGGCTCTCGCTTGTG
AACGCTATCTGAGCGGAGCTAACCTAACGTGGGGCCGACATACCTCCAGCTCGCTTGGG
ATTGAGGTGAATGCCGAGCTAAATTGTCGCTGCCTGGACCCCTGAAGGCAGCAGCCAAGGCT
GCCGCAGTGGTGTGGAGTGGTGTGGATTCAATTCCATGCCCTCACCAAGGCAGTAGAGTG
TGAGGATCC

FIGURE 18K

Prostate 1

LTFWLDRSVKA
AAVLVHPQWVLTVK
AAALLQERGVAYIKA
ALLSIALSVNPLVCNGVLQGVK
AAIMYSAHDTVK
AAAFLTPKKLQCVNAMMNDQLMFLNAGLPSIPVHPV
KAAALGTTCYVGAAI
LLWQPIPVNFLRPRSLQCVKA
FLTSVTWIGVNALLYSLVHN
HLGAATLMSAMTNL

ATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCTGTGGGTGCCGGTCCAGAGGATTG
ACATTTTTGGCTGGATAGATCGGTAAGGCTGCAGCCGTGCTTCACTCCCCAGTGGTCT
TGACCGTAAAGGCTGCCGCCTGCTACAAGAAAGAGGGTCGCATACATCAAAGCTGCTCTC
CTCTTGAGTATTGCGCTAAGTGTAAACCGCTAGTTGTAATGGGTGTTACAAGGTGTGAAA
GCGCGATTATGTACAGTGCACACTACCGTAAAAGCAGCCGCTTCTGACCCAAAA
AAACTCCAATGCGTGAACGCAATGATGAATGATCAGCTGATGTTAAACGCTGGCTTACCT
TCTATAACGGTTCATCCAGTCAGGCGCGCATGGGTACGACGTGTTATGGAGCAGCG
ATACTCTTGGCAGCCATACCAAGTAAATTGTAAGACCTAGATCCTACAATGCGTCAAAG
CATTCCCTACACTCTCAGTAACGGATCGGAGTCAATGCTCTGCTATATAGCCTCGTACACAA
CTTGGCGCGGCCACACTTATGAGTGAATGACGAATTAGCTAAGTCGTGGCGGCCTGGAC
TCTAAAGGCCGAGCA

HIV-1043

MEKVYLA
WPAHK
GIGGGPGP
GQK
QITKI
QNFR
VYYRGP
GPWEF
VNTPPL
V
KLWYQ
GP
PGYR
KILRQR
KIDRL
IDGP
PGP
QHLL
QLTV
WGIK
QLQGP
PG
GEIY
KR
WIIL
GLNK
IVR
MYG
PGP
QGQM
VHQ
AIS
PRT
LN
GP
GI
KQF
IN
MW
QE
VG
KAM
YGP
PG
WAG
IK
QE
FG
I
P
YN
PQ
GP
PG
KT
AV
QMA
VFI
HN
FKR
GP
GP
SPA
IF
QSS
MT
KILE
EP
GP
GE
VN
IV
TD
SQY
ALG
II
GP
GP
HS
N
WR
AM
ASDFNL
PP
GP
GP
GA
ET
FY
VD
GA
AN
RE
TK
GP
GP
GG
AV
VI
QD
NS
DI
K
V
VP
GP
GP
FR
KY
TA
FT
IPS
IN
NE

ATGGAGAACGGTGTACCTGGCCTGGTCCAGCCCACAAAGGCATGGGGAGGGCCGGACC
GGGAGAACAGATACCAAGATCCAGAACTCCGGTATACTACCGGGGACCTGGTCCAG
GTTGGAGTTGTGAACACACCACCTTAGTAAAGCTCTGGTACCGGGCCCGTCCGGAT
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCGGGCCAGGCCAG
CACCTCTGCAGCTACAGTGTGGGAATTAAACAGCTGCAGGGCCGGGCCCCGGGGGGA
AATTATAAAAGGTGGATCATTCTGGTCTGAACAGATCGCCGCATGTATGGCCCTGGACC
CGGACAGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGCCAG
GAATCAAGCAATTCTTAACATGTGGAAGAAGTTGTAAGGCTATGTACGGTCCCGGCCCTG
GATGGGCAGGGATAAAACAGGAGTTGGAATCCCTACAATCCCAGGGTCTGGGCCAGGT
AAAACGGCAGTGCAGATGGCGTGTTCATTCAATTAAAGCGGGGCCCTGGACCTGGCAGC
CCAGCTATATTCAAAGTTCGATGACCAAAATCTGGAGCCCGGCCAGGGCCGGCGAAGT
GAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCGGACCAGGGCATTCAA
TTGGCGGCCATGGCGTGTACTTAATCTACCTCCTGGCCAGGCCCTGGCGCGAAACTTT
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCAGGGCGCTGTAGTCA
TTCAGGACAACCTCAGACATCAAGGTGGTCCCGGTCCAGGCCCGGGTTAGAAAGTATACCG
CCTTCACTATTCCGTCCATCAACAATGAGTGA

FIGURE 18L

HIV-1043 PADRE

MEKVYLAWVPAHKIGGGPGPGQKQITKIQNFRVYYRGPGPGWEFVNTPPLVKLWYQGPGPGYR
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGPGPGGEIYKRWIILGLNKIVRMYGPGPGQGM
VHQAISRTLNGPGPGIKQFINMWQEVGKAMYGPGPGWAGIKQEFGIPYNPQGPGPGKTAVQMA
VFIHNFKRGPGPGSPAIFQSSMTKILEPGPGPGEVNIVTDSQYALGIIGPGPGHSNWRAMASDFNLPP
GPGGAETFYVDGAANRETKGPGPGGAVVIQDNSDIKVVPGPGPGRKYTAFTIPSINNEGPGPA
KFVAATLKA

ATGGAGAAGGTGTACCTGGCTGGTCCAGCCCACAAAGGCATCGGGGGAGGGCCCGGACC
TGGGCAGAACACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG
GTTGGGAGTTGTGAACACACACCCTAGTAAAGCTCTGGTACCAAGGGCCCCGGTCCCGAT
ACCGTAAAATCTGAGGCAAAGAAAGATAGATGCCCTATTGATGGCCCGGGCCCAGGCCAG
CACCTTCTGCAGCTTACAGTGTGGGAATTAAACAGCTGCAGGGGCCGGCCCCGGGGGGA
AATTATAAAAGGTGGATCATCTGGGCTGAACAAGATCGTCCGCATGTATGCCCTGGACC
CGGACAGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTITAATGGACCGGGCCCAG
GAATCAAGCAATTCTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCAGGCTG
GATGGGCAGGGATAAAACAGGAGTTGGAATCCCTACAATCCCCAGGGTCTGGGCCAGGT
AAAACGGCAGTGCAGATGGCGTGTTCATTATAATTAAAGCGGGGCCCTGGACCTGGCAGC
CCAGCTATATTCAAAGTCGATGACCAAAATCTGGAGGCCGCCAGGGCCGGCGAAGT
GAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCAAGGGCATTCAA
TTGGCGGCCATGGCGTCTGACTTTAATCTACCTCTGGGCCAGGCCCTGGCGCGAAACTTT
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAAGGGACCCGGACCCGGCGCTGTAGTCA
TTCAGGACAACACTCAGACATCAAGGTGGTTCCCGTCCAGGGCCGGTTCAAGAAAGTATACCG
CCTCACTATTCCGTCCATCAACAATGAGGGCCCCGGCCAGGTGCCAAGTTCGTGGCTGCCT
GGACCTGAAGGCTGCCGTTGA

HIV 75mer

EKVYLAWVPAHKIGGGPGPGQGMVHQAISRTLNGPGPGSPAIFQSSMTKILEPGPGPGFRKYTA
FTIPSINNE

GAGAAGGTGTACCTGGCTGGTGCCTGCCACAAAGGAATCGGAGGGACCTGGCCCTGGACA
GGGACAGATGGTGCACCAGGCCATCAGCCCTAGGACCTGAACGGACCTGGACCTGGAAAGCC
CTGCCATCTCCAGAGCAGCATGACCAAGATCCTGGAGCCGGACCTGGACCTGGATTCAAGGA
AGTACACCGCCTCACCATCCCCAGCATCAACAACGAGTGA

FIGURE 18M

PfHTL

MQVQIQSLFLLLWVPGSRGRHNWVNHAVPLAMKLIGPGPKCNLYADSAWENVKNGPGPGKS-KYKLATSVLAGLLGPGPGQTNFKSLLRNLVSEGPGPGSSVFNVVNSSLIMGPGPVGKVNIGPFMKAVCVEGPGPGMNYYGKQEENWYSLKGPGPGLAYKFVVPGAATPYGPGPDSIQDSLKESRKLNPGPGPLLIFHINGKIIKNSEGPGPAGLLGNVSTVLLGGVPGPGKYKIAGGIAGGLALLGPGP
GMRKLAILSVSSFLV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGTCCTCCTGTGGGTGCCGGATCCAGA
GGAAGGCACAACACTGGGTGAATCATGCTGTGCCCTGGCTATGAAGCTGATCGGCCCTGGACC
AGGGAAATGCAACCTCTACGCAGACAGCGCCTGGGAGAACGTCAAGAATGGCCCCGGACCTG
GGAATCCAAGTATAAGCTCGCTACCTCTGTGCTGGCAGGCCTGCTGGACCAGGCCCCGGAC
AGACAAATTCAAAGCCTGCTCAGAAACCTGGGAGTGTCCGAGGGGCTGCCAGGATCT
AGCGTCTTAATGTGGTCAACTCCTCTATTGGGCTCATCATGGGACCCGGACCTGGGGTGAAA
AATGTCATTGGCCCATTCATGAAGGCCGTGTGTCGAAGGACCCGGCCTGGCATGAACCTAC
TATGGAAAGCAAGAAAATTGGTACAGCCTGAAGAAAGGCCCTGGGCCAGGCCAGGCGGACTGGCTTA
CAAGTTGTGGTCCCAGGGCAGCCACTCCCTATGGGCTGGGCCAGGCCAGGAACTCCATCCA
GGACTCTCTCAAAGAGAGGCCGGAAACTGAACGGACCCGGCCTGGACTGCTCATTTCCACAT
CAATGGCAAATTATCAAGAACAGCGAGGGACCTGGGCCAGGCCAGGCGCCTGGACTGCTGGGAACG
TGTCCACCGTCCTGCTCGCGGAGTGGGCCCTGGGAAGTACAAGATCGCTGGAGGG
ATCGCAGGCCGGACTGGCCCTCTGGGCCAGGACCAGGGATCGCAAACGGCTATTCTCT
GTCTCCAGCTTCTGTTGTGA

FIGURE 18N

Protein	Sequence	Restriction
HIV gag 386	VLAEAMSQV	HLA-A2
HIV gag 271	MTNNPPIPV	HLA-A2
HIV pol 774	MASDFNLPPV	HLA-A2
HIV pol 448	KLVGKLNWA	HLA-A2
HIV pol 163	LVGPTPVNI	HLA-A2
HIV pol 498	ILKEPVHGV	HLA-A2
HIV pol 879	KAACWWAGI	HLA-A2
HIV pol 132	KMIGGIGGFI	HLA-A2
HIV pol 772	RAMASDFNL	HLA-A2
HIV pol 183	TLNFPISPI	HLA-A2
HIV env 134	KLTPLCVTL	HLA-A2
HIV env 651	LLQLTVWGI	HLA-A2
HIV env 163	SLLNATDIAV	HLA-A2
HIV nef 221	LTFGWCFKL	HLA-A2
HIV vpr 59	AIIIRILQQL	HLA-A2
HIV vpr 62	RILQQLLFI	HLA-A2
HIV pol 929	QMAVFIHNFK	HLA-A3
HIV pol 722	KVYLAWVPAHK	HLA-A3
HIV pol 971	KIQNFRVYYR	HLA-A3
HIV pol 347	AIFQSSMTK	HLA-A3
HIV pol 98	VTIKIGGQLK	HLA-A3
HIV env 61	TTLFCASDAK	HLA-A3
HIV env 47	VTVYYGVPVWK	HLA-A3
HIV nef 100	QVPLRPMTYK	HLA-A3
HIV vif 7	VMIVWQVDR	HLA-A3
HIV gag 162	QMVKHQAISSPR	HLA-A3
HIV gag 545	YPLASLRSLF	HLA-B7
HIV gag 237	HPVHAGPIA	HLA-B7
HIV pol 186	FPISPIETV	HLA-B7
HIV pol 893	IPYNPQSQGVV	HLA-B7
HIV env 259	IPIHYCAPA	HLA-B7
HIV env 250	CPKVSFEPI	HLA-B7
HIV nef 94	FPVRPQVPL	HLA-B7
HIV rev 75	VPLQLPPL	HLA-B7
HIV pol 684	EVNIVTDSQY	HLA-A1
HIV gag 317	FRDYVDRFY	HLA-A1
HIV pol 368	VIYQYMDDLY	HLA-A1
HIV pol 295	TVTLDVGDAY	HLA-A1
HIV pol 533	IYQEPFKNL	HLA-A24
HIV pol 244	PYNTPVFAI	HLA-A24
HIV pol 530	TYQIYQEPEF	HLA-A24
HIV pol 597	YWQATWIPEW	HLA-A24
HIV env 681	IWGCSGKLI	HLA-A24
HIV env 671	RYLKDDQQL	HLA-A24

FIGURE 19A

Protein	Sequence	Restriction
HIV env 55	VWKEATTTLF	HLA-A24
HIV vpr 46	IYETYGDTW	HLA-A24
HIV vpr 14	PYNEWTLEL	HLA-A24
HIV gag 298	KRWIILGLNKIVRMY	HLA-DR
HIV pol 596	WEFVNTPPLVKLWYQ	HLA-DR
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR
HIV pol 712	KVYLAWVPAHKGIGG	HLA-DR
HIV gag 294	GEIYKRWIILGLNKI	HLA-DR
HIV pol 711	EKVYLAWVPAHKGIG	HLA-DR
HIV env 729	QHLLQLTVWGIKQLQ	HLA-DR
HIV gag 171	QGQMVFHQASPRTLN	HLA-DR
HIV pol 335	SPAIFQSSMTKILEP	HLA-DR
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR
HIV pol 303	FRKYTAFTIPSINNE	HLA-DR
HIV pol 758	HSNWARAMASFNLPP	HLA-DR
HIV pol 915	KTAVQMAVFIFHNFKR	HLA-DR
HIV vpu 31	YRKILQRKIDRLID	HLA-DR3
HIV pol 874	WAGIKQEFGIPYNPQ	HLA-DR3
HIV pol 674	EVNIVTDSQYALGII	HLA-DR3
HIV pol 619	AETFYVDGAANRETK	HLA-DR3
HIV pol 989	GAVVIQDNSDIKVVP	HLA-DR3
HCV NS4 1812	LLFNILGGWWV	HLA-A2
HCV NS1/E2 728	FLLLADARV	HLA-A2
HCV NS4 1590	YLVAYQATV	HLA-A2
HCV NS5 2611	RLIVFPDLGV	HLA-A2
HCV CORE 132	DLMGYIPLV	HLA-A2
HCV NS4 1920	WMNRLIAFA	HLA-A2
HCV NS4 1666	VLVGGVLAA	HLA-A2
HCV NS4 1769	HMWNFISGI	HLA-A2
HCV NS4 1851	ILAGYGAGV	HLA-A2
HCV CORE 35	YLLPRRGPRL	HLA-A2
HCV NS1/E2 726	LLFLLLADA	HLA-A2
HCV LORF 1131	YLVTRHADV	HLA-A2
HCV CORE 51	KTSERSQPR	HLA-A3
HCV CORE 43	RLGVRATRK	HLA-A3
HCV ENV1 290	QLFTFSPRR	HLA-A3
HCV NS1/E2 632	RMYVGGVEHR	HLA-A3
HCV NS3 1396	LIFCHSKKK	HLA-A3
HCV NS4 1863	GVAGALVAFK	HLA-A3
HCV NS4 1864	VAGALVAFK	HLA-A3
HCV NS3 1262	LGF GayMSK	HLA-A3
HCV Core 169	LPGCSFSIF	HLA-B7
HCV NS5 2922	LSAFLSHSY	HLA-A1
HCV NS3 1128	CTCGSSDLY	HLA-A1
HCV NS5 2180	LTDPSHITA	HLA-A1

FIGURE 19B

Protein	Sequence	Restriction
HCV Core 126	LTCGFADLMGY	HLA-A1
HCV NS3 1305	LADGGCSGGAY	HLA-A1
HCV NS4 1765	FWAKHMWNF	HLA-A24
HCV NS5 2875	RMILMTHFF	HLA-A24
HCV NS5 2639	VMGSSYGF	HLA-A24
HCV NS4 1765	FWAKHMWNFI	HLA-A24
P. falciparum SSP2-230	FMKAVCVEV	HLA-A2
P. falciparum EXP1-83	GLLGVVSTV	HLA-A2
P. falciparum CSP-7	ILSVSSFLFV	HLA-A2
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3
P. falciparum LSA1-105	GVSENIFLK	HLA-A3
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7
P. falciparum LSA1-1663	LPSENERGY	HLA-A1
P. falciparum EXP1-73	KYKLATSVL	HLA-A24
P. falciparum CSP-12	SFLFVEALF	HLA-A24
P. falciparum LSA1-10	YFILVNLLI	HLA-A24
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2
P. falciparum SSP2-523	LACAGLAYK	HLA-A3
P. falciparum EXP1-10	ALFFIIFNK	HLA-A3
P. falciparum LSA1-11	FILVNLLIFH	HLA-A3
P. falciparum SSP2-126	LPYGRTNL	HLA-B7
P. falciparum CSP-15	FVEALFQEY	HLA-A1
P. falciparum LSA1-1794	FQDEENIGIY	HLA-A1
P. falciparum LSA1-9	FYFILVNLL	HLA-A24
P. falciparum SSP2-8	KYLVIVFLI	HLA-A24
P. falciparum CSP-394	GLIMVLSFL	HLA-A2
P. falciparum EXP1-2	KILSVFFLA	HLA-A2
P. falciparum CSP-344	VTCGNGIQVR	HLA-A3
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1
P. falciparum LSA1-1671	YYIPHQSSL	HLA-A24
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24
P. falciparum LSA1-1881	LFHFIDGDNEI	HLA-A24
P. falciparum CSP-55	YYGKQENWYSL	HLA-A24
P. falciparum LSA1-5	LYISFYFI	HLA-A24
P. falciparum CSP-2	MRKLAILSVSSFLFV	HLA-DR
P. falciparum CSP-53	MNYYGKQENWYSLKK	HLA-DR
P. falciparum CSP-375	SSVFNVVNSSIGLIM	HLA-DR
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3

FIGURE 19C

Protein	Sequence	Restriction
P. falciparum SSP2-223	VKNVIGPFMKAVCVE	HLA-DR
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR
P. falciparum SSP2-527	GLAYKFVVPGAAATPY	HLA-DR
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR
P. falciparum LSA1-16	LLIFHINGKIIKNSE	HLA-DR
P. falciparum LSA1-94	QTNFKSLLRNLGVSE	HLA-DR
HBV core 18	FLPSDFFPSV	HLA-A2
HBV env 183	FLLTRILTI	HLA-A2
HBV env 335	WLSLLVPFV	HLA-A2
HBV pol 455	GLSRYVARL	HLA-A2
HBV pol 538	YMDDVVLGV	HLA-A2/A1
HBV pol 773	ILRGTSFVYV	HLA-A2
HBV pol 562	FLLSLGIHL	HLA-A2
HBV pol 642	ALMPPLYACI	HLA-A2
HBV env 338	GLSPTVWLSV	HLA-A2
HBV core 141	STLPETTVVRR	HLA-A3
HBV pol 149	HTLWKAGILYK	HLA-A3/A1
HBV pol 150	TLWKAGILYK	HLA-A3
HBV pol 388	LVVDFSQFSR	HLA-A3
HBV pol 47	NVSIPWTHK	HLA-A3
HBV pol 531	SAICSVVRR	HLA-A3
HBV pol 629	KVGNFTGLY	HLA-A3/A1
HBV pol 665	QAFTFSPTYK	HLA-A3
HBV core 19	LPSDFFPSV	HLA-B7
HBV env 313	IPIPSSWAF	HLA-B7
HBV pol 354	TPARVTGGVF	HLA-B7
TB	RMSRVTTFTV	HLA-A2
TB	ALVLLMLPVV	HLA-A2
TB	LMIGTAAAVV	HLA-A2
TB	ALVLLMLPV	HLA-A2
TB	GLMTAVYLV	HLA-A2
TB	MALLRLPV	HLA-A2
TB	RMFAANLGV	HLA-A2
TB	SLYFGGICV	HLA-A2
TB	RLPLVLPAV	HLA-A2
TB	RLMIGTAAA	HLA-A2
TB	FVVALIPLV	HLA-A2
TB	MTYAAPLFV	HLA-A2
TB	AMALLRLPLV	HLA-A2
p53 139	KLCPVQLWV	HLA-A2
CEA 687	ATVGIMIGV	HLA-A2
CEA 691	IMIGHLVGV	HLA-A2
Her2/neu 689	RLLQTELV	HLA-A2
MAGE3 112	KVAEIVHFL	HLA-A2

FIGURE 19D

Protein	Sequence	Restriction
Her2/neu 369	KVFGSLAFV	HLA-A2
CEA 605	YLSGANLNV	HLA-A2
MAGE2 157	YLQLVFGIEV	HLA-A2
Her2/neu 665	VVLGVVFGL	HLA-A2
p53 149	SMPPPGTRV	HLA-A2
PAP.21.T2	LTFFWLDRSV	HLA-A2
PAP.112	TLMSAMTNL	HLA-A2
PAP.284	IMYSAHDTTV	HLA-A2
PSM.288.V10	GLPSIPVHPV	HLA-A2
PSM.441	LLQERGVAYI	HLA-A2
PSM.469L2	LLYSLVHNL	HLA-A2
PSM.663	MMNDQLMFL	HLA-A2
PSA.3.V11	FLTLSVTWIGV	HLA-A2
PSA.143.V8	ALGTTCYV	HLA-A2
PSA.161	FLTPKKLQCV	HLA-A2
HuK2.4.L2	LLLSIALSV	HLA-A2
HuK2.53.V11	VLVHPQWVLTW	HLA-A2
HuK2.165	FLRPRSLQCV	HLA-A2
HuK2.216.V11	PLVCNGVLQGV	HLA-A2

FIGURE 19E